

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:49:47 ; Search time 37.7711 Seconds

(without alignments)  
793.576 Million cell updates/sec

Title: US-09-996-617-2\_COPY\_1335\_1429

Perfect score: 490

Sequence: 1 LHFVDQYRQLIARTSVSEV.....HLIMELWKGSKKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_rhiz.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriopl.\*
- 17: sp\_archaeop.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	48.6	195	6 Q8HXK9	Q8HXK9 bos taurus
2	210	42.9	193	11 Q8CHK8	Q8CHK8 rattus norv
3	84.5	17.2	1175	16 Q8XNW6	Q8XNW6 clostridium
4	82.5	16.8	614	16 Q8ENW9	Q8ENW9 oceanobacil
5	79.5	16.2	260	2 Q8GBV1	Q8GBV1 pseudomonas
6	79.5	16.2	260	2 Q8G9V7	Q8G9V7 pseudomonas
7	79.5	16.2	338	2 Q9ZSV9	Q9ZSV9 pseudomonas
8	79.5	16.2	404	2 Q52212	Q52212 pseudomonas
9	79.5	16.2	425	2 Q9X7J2	Q9X7J2 pseudomonas
10	78	15.9	193	17 Q8ZSQ2	Q8ZSQ2 pyrobaculum
11	78	15.9	254	5 Q966F3	Q966F3 caenorhabdi
12	77.5	15.8	376	11 Q8K4E9	Q8K4E9 mus musculu
13	77.5	15.8	376	11 Q921F0	Q921F0 mus musculu
14	76	15.5	295	5 Q95Q18	Q95Q18 caenorhabdi
15	75	15.3	482	16 Q8YKJ7	Q8YKJ7 anabaena sp
16	74.5	15.2	734	2 Q84FL9	Q84FL9 pantoea ag9

17	73.5	15.0	584	16 Q9PLZ8	Q9PLZ8 campylobact
18	73	14.9	376	11 Q8K4E7	Q8K4E7 mus musculu
19	72.5	14.8	630	11 Q8C2K1	Q8C2K1 mus musculu
20	72	14.7	175	16 Q8EPP9	Q8EPP9 oceanobacil
21	72	14.7	376	11 Q8K4E8	Q8K4E8 mus musculu
22	72	14.7	376	11 Q8K4E6	Q8K4E6 mus musculu
23	71.5	14.6	267	5 Q86NF3	Q86NF3 caenorhabdi
24	71.5	14.6	630	11 Q8OXA9	Q8OXA9 mus musculu
25	71	14.5	197	17 Q59062	Q59062 pyrococcus
26	70	14.3	251	11 Q8VI98	Q8VI98 mus musculu
27	70	14.3	252	11 Q8JZN4	Q8JZN4 mus musculu
28	70	14.3	315	11 Q9CP3	Q9CP3 mus musculu
29	70	14.3	376	11 Q8JZN0	Q8JZN0 mus musculu
30	70	14.3	592	16 Q81TV0	Q81TV0 bacillus an
31	70	14.3	691	16 Q8EP55	Q8EP55 mycoplasma
32	70	14.3	870	5 Q9GQ59	Q9GQ59 strongyloce
33	69.5	14.2	96	10 Q8LSL7	Q8LSL7 vitis vinif
34	69.5	14.2	453	13 Q80LR9	Q80LR9 xenopus lae
35	69.5	14.2	609	13 Q92021	Q92021 xenopus lae
36	69	14.1	379	11 Q70522	Q70522 rattus norv
37	69	14.1	406	5 Q17460	Q17460 schistosoma
38	69	14.1	788	12 Q91NQ3	Q91NQ3 prune dwarf
39	69	14.1	870	2 Q84HV6	Q84HV6 anaplasma m
40	69	14.1	871	16 Q9XIR4	Q9XIR4 thermotoga
41	68.5	14.0	610	13 Q91431	Q91431 xenopus lae
42	68.5	14.0	771	13 Q918K4	Q918K4 rana catesb
43	68	13.9	265	16 Q81GN8	Q81GN8 bacillus ce
44	68	13.9	368	10 Q41236	Q41236 solanum tub
45	68	13.9	1816	12 Q91WB1	Q91WB1 soil-borne

#### ALIGNMENTS

#### RESULT 1

Q8HXK9 PRELIMINARY; PRT; 195 AA.

AC Q8HXK9, TREMBLrel. 23, Created)  
DT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-WAR-2003 (TREMBLrel. 24, Last annotation update)  
DE Apoptosis-associated speck-like protein containing a CARD.  
GN BASC.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,  
RA Katsuyama T., Sagara J., Taniguchi S., Ngo-Hazelett P.,  
RA Postlethwait J.H., Nunez G., Inohara N.,  
RT "Casp-1: A zebrafish caspase activated by ASC oligomerization required  
RT for pharyngeal Arch development.";  
RL J. Biol. Chem. 274:33835-33838(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20036508; PubMed=10567338;  
RA Masumoto J., Taniguchi S., Ayukawa K., Sarvotham H., Kishino T.,  
RA Nishikawa N., Hidaka E., Katsuyama T., Higuchi T., Sagara J.,  
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human  
RT promyelocytic leukemia HL-60 cells.";  
RL J. Biol. Chem. 274:33835-33838(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20580347; PubMed=11139337;  
RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.,  
RT "Murine ortholog of ASC, a CARD-containing protein, self-associates,  
RT and exhibits restricted distribution in developing mouse embryos.";  
RL Exp. Cell Res. 262:128-133(2001).  
DR EMBL; AB050006; BAC43753.1;  
DR GO; GO:0005622; Cintracellular; IEA.







```
Db      83 GLFQCXDG---QURFVHPFSNQLLASHERRGLFP 115  
          :|||:::||:||||:  
  
RESULT 12  
QBK4E9  
ID       Q8K4B9              PRELIMINARY;           PRT;    376 AA.  
AC       Q8K4E9;  
DT       01-OCT-2002 (TrEMBLrel. 22, Created)  
DT       01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE       01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE       2'-5' oligoadenylate synthetase 1B.  
GN       OAS1B.  
OS       Mus musculus (Mouse).  
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX       NCBI_TaxID=10090;  
RN       [1]  
RP       SEQUENCE FROM N.A.  
RC       STRAIN=MOLD/Rk;  
RX       MEDLINE=22103633; PubMed=12080145;  
RA       Parolylin A.A., Scherbik S.V., Zhulin I.B., Stockman B.M., Li Y.,  
RA       Bincon M.A.; F. antib. vital response protein activity; IDA.  
RT       "Positional cloning of the murine flavivirus resistance gene."  
RL       Proc. Natl. Acad. Sci. U.S.A. 93:9327-9327(2002) .  
DR       ENBL; AF418006; AAM47546.1 ; -.  
MGD; MGJ:197430; Oaslb.  
DR       GO: 0003380; F:antiviral response protein activity; IDA.  
DR       InterPro; IPRO06117; 2SA_SYNTH_2.  
DR       InterPro; IPRO06116; 2SA_synth_UB.  
DR       InterPro; IPRO01201; PAP_25A_core.  
DR       PROSITE; PS00833; 2SA_SYNTH_2; 1.  
DR       PROSITE; PS0152; 2SA_SYNTH_3; 1.  
SQ       SEQUENCE 376 AA; 43919 MW; CFA34CABC3874842 CRC64;
```

Query Match            15.8%; Score 77.5; DB 11; Length 376;  
Best Local Similarity     28.3%; Pred No. 8.2;  
Matches        26; Conservative      17; Mismatches    40; Indels      9; Gaps      3

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QY     1 LHFVDGYREQLIARVTISVEVLDKLGSQLVSQSQRYERVALENTSPQRKLFSLSQSWDR 60  
DB     155 LNLIKPNQQFYANLTSGRTPGKG-EKKLLTCFWMLRGKYFLNCRRPTKLRILRLVTHWYQ 213  
               :::::::::::::::::::::  
QY     61 KCKOGLYOALKETHPLHLMEL-----WEKGSK 87  
               ||::|::|::|::|::|::|::|::  
DB     214 LCKEKIGDPLP--PQVALSLTVYAWEYGSR 242  
               |::|::|::|::|::|::|::|:
```

RESULT 13  
Q921FO  
ID Q921FO PRELIMINARY; PRT; 376 AA.  
AC Q921FO;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to 2'-5' oligoadenylate synthetase 1B (2'-5'-oligoadenylate  
DE synthetase 1).  
GN OASIA OR OASI.  
OS Mus musculus (Mouse), and  
OS Mus musculus musculus (eastern European house mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090, 39442;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Mouse;  
RA Strausberg R.;  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBSJ databases.

[2]

```
RN       SEQUENCE FROM N.A.  
RP       SPECIES=m.m.musculus; STRAIN=MBT/Pas;  
RX       MEDLINE=42177231; PubMed=12186974;  
RA       Mashimo T., Lucas M., Simon-Chazottes D., Frankiel M.P.,
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RA Montagutelli X., Ceccaidi P.E., Deubel V., Guenet J.L., Despres P.;
RT "A nonsense mutation in the gene encoding 2'-5'-oligoadenylate
RT synthetase/L1 isoform is associated with West Nile virus
RT susceptibility in laboratory mice."
RL Proc. Natl. Acad. Sci. U.S.A. 99:11311-11316(2002).
DR EMBL; BC012877; AAH12877.1; -
DR EMBL; AF466823; AAM37604.1; -
DR MGB; MGI:2180860; Oasia.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006117; 2SA_SYNTH_2
DR InterPro; IPR006116; 2SA_SYNTH_US
DR InterPro; IPR001201; PAP_2SA_core.
DR PROSITE; PS00833; 2SA_SYNTH_2; 1.
DR PROSITE; PS0152; 2SA_SYNTH_3; 1.
DR PROSITE; PS0152; 2SA_SYNTH_3; 1.
SQ SEQUENCE 376 AA; 43934 MW; 30F970452408FB7E CRC64;

Query Match 15.8%; Score 77.5; DB 11; Length 376;
Best Local Similarity 28.3%; Pred. No. 8.2; Mismatches 40; Indels 9; Gaps 3;
Matches 26; Conservative 17;

QY 1 LHFVDQREQLIARTVSVVVDLKHQVLSQEQYERVLAEINTRPSQMRKLFSLQSQWDR 60
DB 155 LNILKPKNQFYANLISGRTEPLGR-EGKLLTCFWMGLRKYFLNCRPTKELIHLVTHWYQ 213
QY 61 KCKDGLVQALKETHPHLIMEL-----WEKSK 87
DB 214 LCKEKLGDPLP---POVALELLTYAWEYGSR 242

RESULT 14
Q95Q18 PRELIMINARY; PRT; 295 AA.
AC Q95Q18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Y53F4B.39 protein.
CN Y53F4B.39
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Smye R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; ALI32949; CAB61094.1; -
DR WormPep; Y53F4B.39; CE24418.
DR InterPro; IPR001279; Blackmase-like.
DR Pfam; PF00753; lactamase B; 1.
SQ SEQUENCE 295 AA; 33102 MW; 5D798FC5C67B97CB CRC64;

Query Match 15.5%; Score 76; DB 5; Length 295;
Best Local Similarity 26.7%; Pred. No. 8.8;
Matches 23; Conservative 17; Mismatches 40; Indels 6; Gaps 2;

QY 4 VDQYREQLIARTVSVVVDLKHQVLSQEQYERVLAEINTRPSQMRKLFSLQSQWDRKCK 63
DB 206 VDEIEHMKREERIIKVL-KEHEITSMQVYADSPWAVELALNNVNLVKKLCK 264
QY 64 DGLYQALKETHPHLIMELWEKSK 89.
DB 265 DGVEE-----NPFETFKWIGSSSG 285

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## RESULT 15

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Q8YKJ7 PRELIMINARY; PRT; 482 AA.
AC Q8YKJ7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ALR7298.
GN ALR7298.
OS Anabaena sp. (strain PCC 7120).
OG Plasmid pCC7120alpha.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RA "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003600; BAB78382.1; -
DR FIR; AB2515; AB2515
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015428; F:type I protein secretor activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR003997; RtxD.
DR PRINTS; PR01490; RTXTOXIND.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 482 AA; 54120 MW; 95E4C016A9CF66A CRC64;

Query Match 15.3%; Score 75; DB 16; Length 482;
Best Local Similarity 24.1%; Pred. No. 20;
Matches 21; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 15 VTSVEVVDLKHQVLSQEQYERVLAEINTRPSQMRKLFSLQSQWDRKCKDGLYQALKETH 74
DB 258 ITQINAELEKLNTRSKQLEQ-NNLAAADNTENNQIQELQQAIRWEKEVADN--STIKSS 314
QY 75 PHLMEL-----WEKSKGLPLS 94
DB 315 AGCIVEITATLQGLSPGNRLGTLQIS 341

```

Search completed: July 28, 2004, 08:54:45

Job time : 39.7711 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:37 ; Search time 9.15663 Seconds  
(without alignments)  
540.228 Million cell updates/sec

Title: US-09-996-617-2\_COPY\_1335\_1429

Perfect score: 490

Sequence: 1 LHFVDQYRQLIARTSVSEV.....HLIMELWEKSGKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	100.0	1473	1	NALL_HUMAN
2	253	51.6	193	1	ASC_MOUSE
3	236	48.2	195	1	ASC_HUMAN
4	96	19.6	203	1	ASC_BRARE
5	94.5	19.3	431	1	CAR8_HUMAN
6	75	15.3	349	1	OAS1_PIG
7	73.5	15.0	1260	1	LINI_NYCCO
8	72	14.7	953	1	CAR4_HUMAN
9	72	14.7	953	1	CAR4_MOUSE
10	72	14.7	1087	1	OAS3_HUMAN
11	71	14.5	833	1	SYL_STRPN
12	70	14.3	192	1	OASB_MOUSE
13	70	14.3	494	1	ENP2_CHICK
14	69.5	14.2	400	1	OAS1_HUMAN
15	69	14.1	833	1	SYL_STRK6
16	68	13.9	1034	1	PGAL_BACME
17	67.5	13.8	204	1	VNSC_PIIHB
18	67.5	13.8	204	1	VNSC_PIIHE
19	67.5	13.8	344	1	FLIG_BORBU
20	66.5	13.6	200	1	VIP_CHICK
21	66.5	13.6	468	1	SFE_THERTH
22	66	13.5	455	1	2PFI_CASEEL
23	66	13.5	804	1	SYL_STAAM
24	66	13.5	807	1	SYL_STAAM
25	66	13.5	833	1	SYL_STRP8
26	65.5	13.4	322	1	VQJA_BACSU
27	65.5	13.4	430	1	ACDL_PIG
28	65.5	13.4	1102	1	MISC_CHICK
29	65	13.3	358	1	OAS1_RAT
30	65	13.3	454	1	CPK2_MOUSE
31	65	13.3	779	1	PHK2_RHIME
32	65	13.3	1242	1	NPHN_MOUSE
33	64.5	13.2	430	1	ACDL_HUMAN

34 64 13.1 367 1 OASA\_MOUSE  
35 64 13.1 509 1 AURE\_STAAR  
36 64 13.1 833 1 SYL\_STRMU  
37 64 13.1 1182 1 HAIR\_MOUSE  
38 63.5 13.0 204 1 VNSC\_PIIHD  
39 63.5 13.0 539 1 RIK2\_MOUSE  
40 63.5 13.0 611 1 BIR\_CHICK  
41 63.5 13.0 724 1 P85A\_HUMAN  
42 63.5 13.0 749 1 SPOT\_SPICI  
43 63.5 13.0 1178 1 RPOB\_TREPA  
44 63 12.9 411 1 SYS\_CAMEJ  
45 63 12.9 4466 1 DYHC\_ANTCR

## ALIGNMENTS

RESULT 1  
NALL\_HUMAN  
ID NALL\_HUMAN STANDARD; PRT: 1473 AA.  
AC Q9C000; Q9BZ28; Q9BZ29; Q9HAV8; Q9UFT4; Q9V2E0;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE NACT-, LRR- and PYD-containing protein 2 (Death effector filament-forming ced-4-like apoptosis protein) (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7).  
DE forming ced-4-like apoptosis protein (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7).  
GN NALF1 OR DEFCAP OR NAC OR CARD7 OR KIAA0926.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=21169419; PubMed=11270363;  
RA Bertin J., Distefano P.S.;  
RT "The PYRIN domain: a novel motif found in apoptosis and inflammation proteins.";  
RT Cell Death Differ. 7:1273-1274 (2000).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=21148093; PubMed=11250163;  
RA Martinon F., Hoffmann K., Tschoep J.;  
RT "The pyrin domain: a possible member of the death domain-fold family implicated in apoptosis and inflammation.";  
Curr. Biol. 11:R118-R120 (2001).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX TISSUE=Erythrocytopenia;  
RX MEDLINE=21153743; PubMed=11076957;  
RA Hlaing T., Guo R.-F., Dilley K.A., Loussia J.M., Morrish T.A., Shi M.M., Vincenz C., Ward P.A.;  
RT "Molecular cloning and characterization of DEFCAP-L and -S, two isoforms of a novel member of the mammalian Ced-4 family of apoptosis proteins.";  
J. Biol. Chem. 276:9230-9238 (2001).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2; 3 AND 4), AND PROTEIN INTERACTION.  
RX TISSUE=T-cell;  
RX MEDLINE=21153744; PubMed=11113115;  
RA Chu Z.-L., Pio F., Xie Z., Welsh K., Krajewska M., Krajewski S., Godzik A., Reed J.C.;  
RT "A novel enhancer of the Apaf1 apoptosome involved in cytochrome c-dependent caspase activation and apoptosis.";  
J. Biol. Chem. 276:9239-9245 (2001).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX TISSUE=Brain;  
RX MEDLINE=99246063; PubMed=10231032;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroasawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code

RT for large proteins in vitro. ";

RL DNA Res. 6:63-70(1999).

RN [6]

RP SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1).

RC TISSUE=Uterus;

RA Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;

RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Able to form cytoplasmic structures termed death

CC effector filaments. Enhances APA1 and cytochrome c-dependent

CC activation of pro-caspase-9 and consecutive apoptosis. Seems to

CC bind ATP.

CC -!- SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9

CC and with APA1 in a cytochrome c-inducible way leading to the

CC formation of an apoptosome. This interaction may be ATP-dependent.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=4;

CC Name=1; Synonyms=NAC beta, DEFCAP-L;

CC IsoId=Q9C000-1; Sequence=Displayed;

CC Name=2; Synonyms=NAC alpha, DEFCAP-S;

CC IsoId=Q9C000-2; Sequence=VSP\_004327;

CC Name=3; Synonyms=NAC gamma;

CC IsoId=Q9C000-3; Sequence=VSP\_004326, VSP\_004327;

CC Name=4; Synonyms=NAC delta;

CC IsoId=Q9C000-4; Sequence=VSP\_004326;

CC -!- TISSUE SPECIFICITY: Widely expressed. Isoforms 1 and 2 are

CC expressed in peripheral blood leukocytes, chronic myelogenous

CC leukemia cell line K-562, followed by thymus, spleen and heart.

CC Also detected in lung, placenta, small intestine, colon, kidney,

CC liver and muscle.

CC -!- SIMILARITY: Contains 1 DAPIN domain.

CC -!- SIMILARITY: Contains 1 NACHT domain.

CC -!- SIMILARITY: Contains 1 CARD domain.

CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.

CC -----

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CC -----

DR EMBL; AF298548; AAG15254.1; -

DR EMBL; AF310105; AAG30288.1; -

DR EMBL; AF229059; AAK00748.1; -

DR EMBL; AF229060; AAK00749.1; -

DR EMBL; AF229061; AAK00750.1; -

DR EMBL; AF229062; AAK00751.1; -

DR EMBL; AB023143; BAA76770.1; -

DR EMBL; AL117470; CAB55945.1; -

DR PIR; T17255; T17255.

DR HSSP; PI3489; I44Y.

DR MIM; 606636; -

DR GO; GO:0005622; C:intracellular; IC.

DR GO; GO:0016506; F:apoptosis activator activity; NAS.

DR GO; GO:0008656; F:gaspase activator activity; NAS.

DR GO; GO:0019899; F:enzyme binding; IPI.

DR GO; GO:0006919; P:gaspase activation; NAS.

DR GO; GO:0006917; P:induction of apoptosis; NAS.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR000767; Disease\_resist.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR007091; LRR\_Rninh.

DR InterPro; IPR007111; NACHT\_NUPase.

DR InterPro; IPR004020; PAAD\_DAPIN\_dom.

DR Pfam; PF00560; LRR; 2.

DR Pfam; PF05729; NACHT; 1.

DR Pfam; PF02758; PAAD\_DAPIN; 1.

DR PRINTS; PR00364; DISEASERIST.

DR PROSITE; PS50209; CARD; 1.

DR PROSITE; PS50824; DAPIN; 1.

DR PROSITE; PS50837; NACHT; 1.

KW Apoptosis; ATP-binding; Leucine-rich repeat; Repeat;

FT Alternative splicing

FT DOMAIN 328 637 DAPIN.

FT REPEAT 704 725 NACHT.

FT REPEAT 807 830 LRR 1.

FT REPEAT 864 887 LRR 2.

FT REPEAT 921 944 LRR 3.

FT REPEAT 950 973 LRR 4.

FT REPEAT 1199 1215 LRR 5.

FT REPEAT 1216 1236 LRR 6.

FT REPEAT 1374 1463 LRR 7.

FT DOMAIN 1374 1463 CARD.

FT NP\_BIND 334 341 ATP (POTENTIAL).

FT VARSPPLIC 958 987 Missing (in isoform 3 and isoform 4).

FT VARSPPLIC 1262 1305 Missing (in isoform 2 and isoform 3).

FT MUTAGEN 340 340 /FTId=VSP\_004327.

FT MUTAGEN 340 340 K->L: NO EFFECT.

FT CONFLICT 155 155 K->S: NO EFFECT.

FT CONFLICT 246 246 L -> H (IN REF. 1).

FT CONFLICT 782 782 T -> S (IN REF. 1).

FT CONFLICT 878 878 T -> S (IN REF. 1).

FT CONFLICT 878 878 T -> M (IN REF. 1).

FT CONFLICT 995 995 T -> I (IN REF. 1).

FT CONFLICT 1119 1119 M -> V (IN REF. 1).

FT CONFLICT 1184 1184 M -> V (IN REF. 1 AND 6).

FT CONFLICT 1241 1241 V -> L (IN REF. 1).

FT CONFLICT 1366 1366 R -> C (IN REF. 1).

SQ SEQUENCE 1473 AA; 165865 MW; 438F0DCE45C2562D CRC64;

Query Match 100.0%; Score 490; DB 1; Length 1473;

Best Local Similarity 100.0%; Pred. No. 1.7e-40;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYVERVLAENTRPSQMRKLFSLSQSWDR 60

Db 1379 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYVERVLAENTRPSQMRKLFSLSQSWDR 1438

QY 61 KCKDGLYQALKEHPHLMELWEGSKKGLPLSS 95

Db 1439 KCKDGLYQALKEHPHLMELWEGSKKGLPLSS 1473

RESULT 2

ASC\_MOUSE STANDARD; PRT; 193 AA.

ID Q9EPB4; Q9D2W9;

AC Q9EPB4; Q9D2W9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Apoptosis-associated speck-like protein containing a CARD (mASC)

DE (PYCARD).

GN ASC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=BAJB/c; TISSUE=Thymus;

RX MEDLINE=20580347; PubMed=11139337;

RA Muramoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.;

RT "Murine ortholog of ASC, a CARD-containing protein, self-associates

RT and exhibits restricted distribution in developing mouse embryos.";

RL Exp. Cell Res. 262:128-133(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Breast tumor;

RA Martinon F., Hofmann K., Tschopp J.;

RT "PyCard a PYD and CARD containing molecule.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.



RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Tongue;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saigo R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,  
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima G., Mazzarelli I., Sakamoto N.,  
RA Nordone P., Ring B., Schoenbach C., Segura T., Shibata Y., Storch K.F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyszynski B.A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic  
activity is mediated predominantly through the activation of  
caspase 9 (by similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,  
a redistribution from the cytoplasm to the aggregates occurs.  
CC These aggregates are hollow, perinuclear spherical, ball-like  
structures (by similarity).  
CC -1- TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus,  
spleen, brain, heart, skeletal muscle, kidney, lung and liver.  
CC -1- DEVELOPMENTAL STAGE: Strongly expressed at E9.5 day in the  
telencephalon, thalamic areas of the diencephalon, heart and  
liver.  
CC -1- SIMILARITY: Contains 1 DAPIN domain.  
CC -1- SIMILARITY: Contains 1 CARD domain.  
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DR EMBL; AB032249; BAB16609.1; -;  
DR EMBL; AF310104; AAG30287.1; -;  
DR EMBL; AK009852; BAB26543.1; -;  
DR EMBL; AK007742; BAB25229.1; -;  
DR EMBL; AK018682; BAB31341.1; -;

DR EMBL; BC008252; AAH08252.1; -;  
DR MGD; MGI:1931465; Asc.  
DR GO; GO:0005829; C:cytosol; IDA.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR004020; PAAD\_DAPIN\_dom.  
DR Pfam; PF02758; PAAD\_DAPIN\_1.  
DR PROSITE; PS02029; CARD; 1.  
DR PROSITE; PS0824; DAPIN; 1.  
KW Apoptosis; Anti-oncogene.  
FT DOMAIN 1 91 DAPIN.  
FT DOMAIN 105 193 CARD.  
FT CONFLICT 159 159 K -> E (IN REF. 3).  
SQ SEQUENCE 193 AA; 21458 MW; 2A4EA40194870B31 CRC64;  
Query Match 51.6%; Score 253; DB 1; Length 193;  
Best Local Similarity 61.2%; Pred.No. 4.6e-18;  
Matches 49; Conservative 11; Mismatches 20; Indels 0; Gaps 0;  
QY 2 HFVDQYREQLARTVSEVVLDKLGVLSQEQYERVLAEINTREPSQMRKLFSLSQSDRK 61  
DB 111 HFVDQHQLARTVEVDGLDGLGSLVTEGQVAVRAETTSQDKKRLFSFVPSNLT 170  
QY 62 CKDGLYQALKETHPHLIMEL 81  
DB 171 CKDSLLQALKEIHFVYVMDL 190  
RESULT 3  
ASC\_HUMAN STANDARD; PRT; 195 AA.  
ID ASC\_HUMAN Q9UJZ3; Q96D12; Q9BSZ5; Q9HBD0; Q9NXJ8;  
AC 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Apoptosis-associated speck-like protein containing a CARD (hASC)  
DE (PYCARD) (target of methylation-induced silencing 1) (Caspase  
DE recruitment domain protein 5).  
DE ASC OR TMS1 OR CARDS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX TISSUE=Leukemia;  
RX MEDLINE=20035508; PubMed=10567338;  
RA Masumoto J., Taniguchi S., Ayukawa K., Sarvatham H., Kishino T.,  
RA Nikiwa N., Hidaka E., Katsuyama T., Higuchi T., Sagara J.;  
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human  
RT promyelocytic leukemia HL-60 cells.";  
RL J. Biol. Chem. 274:33835-33838(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Fibroblast;  
RX MEDLINE=20552139; PubMed=11103776;  
RA Conway K.E., McConnell B.B., Bowring C.E., Donald C.D., Warren S.T.,  
RA Vertino P.M.;  
RT "TMS1, a novel proapoptotic caspase recruitment domain protein, is a  
RT target of methylation-induced gene silencing in human breast  
RT cancers";  
RL Cancer Res. 60:6236-6242(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Martinon F., Hofmann K., Tschopp J.;  
RT "PyCard a PYD and CARD containing molecule";  
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Bertin J.;  
RT "CARD5 protein is a CARD/PYRIN family member that is involved in  
RT apoptosis signal transduction.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]



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CC -----
CC EMBL; AF231013; AAF66956.1; -.
CC ZFIN; ZDB-GENE-000511-2; asc1.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR004020; PAAD_DAPIN_dom.
CC Pfam; PF02758; PAAD_DAPIN; 1.
CC PROSITE; PS0209; CARD; 1.
CC PROSITE; PS0824; DAPIN; 1.
CC Apoptosis; Anti-oncogene.
CC KW
CC DOMAIN 1 91 DAPIN.
CC FT
CC DOMAIN 112 203 CARD.
CC SEQUENCE 203 AA; 22867 MW; EF457179EB7A78A7 CRG64;

Query Match 19.6%; Score 96; DB 1; Length 203;
Best Local Similarity 31.3%; Pred.No. 0.016;
Matches 26; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

QY 1 LHFVDYQEQIARVTSVEVLDKL-HGVLSQEQYERVLAENTRPSOMKLFSLSQSW- 58
DB 117 VNFIDEHWKEJLDRVNNVPDILROKKVITNEDYCTIRNKETPOKKRELLTGPITCA 176
QY 59 DRKCKDGLYQALKETHPELIMEL 81
DB 177 GNKGVEVLYDALRESNKFIMDDL 199

RESULT 5
CAR8_HUMAN
ID CAR8_HUMAN STANDARD; PRT; 431 AA.
AC Q9Y2G2; Q96P82;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 8 (Apoptotic protein NDPPI) (DACA)
DE (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (TUCAN).
DE CAR8 OR NDPPI OR KIAA0955.
DE Homo sapiens (Human).
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX TISSUE=Brain;
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RA DiStefano P.S., Bertin J., Alnemri E.S.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=21950691; PubMed=11821383;
RA Razmara M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,
RA DiStefano P.S., Bertin J., Alnemri E.S.;
RT "CARD-8 protein, a new CARD family member that regulates caspase-1
RT activation and apoptosis.";
RL J. Biol. Chem. 277:13952-13958(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX Zhang H.;
RT "A novel apoptotic protein, NDPPI, containing CARD and BH3 domains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX Guet C., Vito P.;
RT "DACA, a novel CARD-containing protein.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM LONG).

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FT CONFLICT 422 422 L -> P (IN REF. 5).
SQ SEQUENCE 431 AA; 48932 MW; CB54D13080773256 CRC64;

Query Match
Best Local Similarity 19.3%; Score 94.5; DB 1; Length 431;
Matches 26; Conservative 17; Mismatches 36; Indels 1; Gaps 1;

QY 3 FVDQYREQLIAVTSVEVLDKLH-GOVLSEQYVERVLAENTRPSQMRKLFSLSQSWDRK 61
DB 347 PVKENHRQLQRMGDLKQVLDLQDNVLTENKELVEQKTRQSKNEALLSWVEKKGDL 406

QY 62 CKQGLYQALKETHPHLIMEL 81
DB 407 ALDVLFRSISERDPVLSYL 426

RESULT 6
OAS1_PIG
ID OAS1_PIG STANDARD; PRT; 349 AA.
AC Q29599; O77734;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 2'-5'-oligoadenylate synthetase 1 (EC 2.7.7.-) ((2-5')oligo(A)
synthetase 1) (2-5A synthetase 1) (p42 OAS).
GN OAS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Small intestine;
RA Hartmann R.;
RL Thesis (1997), University of Aarhus, Denmark.
[2]
RP SEQUENCE OF 1-128 FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS
INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.
CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP
into PPP(A2'P5'A)N oligomers, which activate the latent RNase L
that, when activated, cleaves single-stranded RNAs.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR
FRACTIONS SUCH AS MITOCHONDRIAL, NUCLEAR, AND ROUGH/SMOOTH
MICROSOMAL FRACTIONS (By similarity).
CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.
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DR EMBL; AJ225090; CAA12397.1;
DR EMBL; F14610; CAA23153.1; ALT INIT.
DR InterPro; IPR006117; 25A_SYNTH_2.
DR InterPro; IPR006116; 25A_synth_US.
DR InterPro; IPR001201; PAP_25A_core.
DR PROSITE; PS00832; 25A_SYNTH_1; 1.
DR PROSITE; PS00833; 25A_SYNTH_2; 1.
DR PROSITE; PS0152; 25A_SYNTH_3; 1.
KW RNA-binding; Transferase; Nucleotidyltransferase;
Interferon induction.
FT CONFLICT 54 54 V -> F (IN REF. 2).
```

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FT CONFLICT 122 122 S -> R (IN REF. 2).
SQ SEQUENCE 349 AA; 40246 MW; 06949A35BFCF7710 CRC64;

Query Match
Best Local Similarity 15.3%; Score 75; DB 1; Length 349;
Matches 18; Conservative 9; Mismatches 10; Indels 18; Gaps 3;

QY 44 RPSQMRKLFSLSQSWDRKCKDGLYQALKETH-----PHLIMEL-----WEKGSKK 88
DB 200 RRTKLKSLRLVKHW-----YQCKTKHGNKLPPOVALELLTVYAWEQGSRK 246

RESULT 7
LIN1_NYCCO
ID LIN1_NYCCO STANDARD; PRT; 1260 AA.
AC P08548;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DE LINE-1 reverse transcriptase homolog.
OS Nycticebus coucang (Slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
SEQUENCE.
RP MEDLINE=86230917; PubMed=2423883;
RA Hattori M., Kuhara S., Takenaka O., Sakaki Y.;
RT "L1 family of repetitive DNA sequences in primates may be derived
from a sequence encoding a reverse transcriptase-related protein.";
RL Nature 321:625-628(1986).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS CONSTRUCTED FROM AN ALIGNMENT OF
SIX SEQUENCES, DETERMINED BY THESE AUTHORS BUT NOT SHOWN,
BELONGING TO THE LINE-1 FAMILY.
CC PIR; B25313; GNLR1.
CC DR HSSP; P27695; 1HD7.
CC DR InterPro; IPR005135; Exo_endo_phos.
CC DR InterPro; IPR000477; RVTSe.
CC DR Pfam; PF03372; Exo_endo_phos; 1.
CC DR Pfam; PF00078; rvt; 1.
CC DR RNA-directed DNA polymerase.
KW SEQUENCE 1260 AA; 147042 MW; 7A6803DF471F7253 CRC64;

Query Match
Best Local Similarity 15.0%; Score 73.5; DB 1; Length 1260;
Matches 23; Conservative 24; Mismatches 38; Indels 15; Gaps 3;

QY 4 VDQYREQLIA----RVTSVEVLDKLHGQVLSEQYVERVLAENTRPSQMRKLFSLSQSWD 59
DB 410 LNEYKLYSHKYENLKIDQVLEACHLPRLSQKEVEML----NRPISSEIASTIQNLQ 465

QY 60 RKCKDG-----LYQALKETHPHLIMELWEKSKKGLLP 92
DB 466 KKKSPGPGDFTSEFYQTFRKLVPILLNLFQNIKEGILP 505

RESULT 8
CAR4_HUMAN
ID CAR4_HUMAN STANDARD; PRT; 953 AA.
AC Q9Y39; Q81WFS;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 4 (Nod1 protein).
GN CARD4 OR NOD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Endothelial cells;
RC MEDLINE=99240667; PubMed=10224040;
RX
```

Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R., Grant J.R., Kelly J.J., Gosselin M.L., Robison K.E., Wong G.H.W., Glucksmann M.A., Distefano P.S.;  
RA "Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member  
RA that activates NF-kappaB";  
RT J. Biol. Chem. 274:12955-12958(1999).  
RL [2]  
RV  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.  
RR TISSUE=Breast;  
RZ MEDLINE=99262599; PubMed=10329646;  
RX Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R., Merino J., Liu D., Ni J., Nunez G.;  
RA "Nod1, an Apaf-1-like activator of caspase-9 and nuclear factor-  
RA kappaB";  
RT J. Biol. Chem. 274:14560-14567(1999).  
RL [3]  
RV  
RP SEQUENCE FROM N.A.  
RR TISSUE=Lymph;  
RZ MEDLINE=22388257; PubMed=12477932;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhac N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoig F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.U., Hulyk S.W., Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.Z., Jones S.J.M., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RV [4]  
RP FUNCTION  
RR MEDLINE=21264704; PubMed=11058605;  
RX Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;  
RA "Human Nod1 confers responsiveness to bacterial lipopolysaccharides.";  
RT J. Biol. Chem. 276:2551-2554(2001).  
RL [-] FUNCTION: Enhances caspase-9-mediated apoptosis. Induces NF-kappa-B activity via RICK (CARDIAC, RIP2) and IKK-gamma. Confers responsiveness to intracellular bacterial lipopolysaccharides (LPS).  
RV [-] SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD interaction.  
RR [-] SUBCELLULAR LOCATION: Cytoplasmic.  
RX [-] TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal muscle, pancreas, spleen and ovary. Also detected in placenta, lung, liver, kidney, thymus, testis, small intestine and colon.  
CC [-] SIMILARITY: Contains 1 CARD domain.  
CC [-] SIMILARITY: Contains 1 NACHT domain.  
CC [-] SIMILARITY: Contains 9 leucine-rich (LRR) repeats.  
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RL -----  
RV EMBL; AF126484; AAD29125.1; -  
RR EMBL; AF149774; AAD43922.1; -  
RX EMBL; AF113925; AAD28350.1; -  
RY EMBL; BC040339; AAH04339.1; -  
RZ Genew; HGNC:16390; CARD4.  
RV MIM; 605980; -

DR	GO: GO:000656; F.caspase activator activity; TAS.
DR	GO: GO:0006915; P.apoptosis; TAS.
GO	GO: GO:0007165; P.signal transduction; TAS.
DR	Inter-Pro; IPR001315; CARD.
DR	Inter-Pro; IPR007091; LRR_RNinh.
DR	Inter-Pro; IPR007111; NACHT_NTPase.
DR	Pfam; PF00619; CARD; 1.
DR	Pfam; PF05729; NACHT; 1.
DR	PROSITE; PS0209; CARD; 1.
DR	PROSITE; PS0837; NACHT; 1.
KW	Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.
FT	DOMAIN 15 105
FT	DOMAIN 196 531
FT	NP_BIND 202 209
FT	REPEAT 632 656
FT	REPEAT 702 725
FT	REPEAT 727 750
FT	REPEAT 755 778
FT	REPEAT 783 806
FT	REPEAT 839 862
FT	REPEAT 867 891
FT	REPEAT 895 918
FT	REPEAT 923 946
FT	MUTAGEN 41 41
FT	MUTAGEN 208 208
FT	CONFLICT 447 447
FT	SEQUENCE 953 AA; 107630 MW; 0A9DF5FC6487E21A CRC64; .
QY	8 REQLIARVTSVEVLDBK-LHGQVLSQEQVERVLAENTRFSQMRKFLSLSQSDRKCKD-- 64
Db	27 RELVTHIRNTQCLVNILNLDYFSDEAETVCACPTQDKVKILDLVQSKGEVSEFF 86
QY	65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
Db	87 LYLQLQADAYVDLRPWLLEIGFSPSLITQS 117
RESULT 9	
CAR4 MOUSE	
ID	CAR4 MOUSE STANDARD; PRT; 953 AA.
AC	Q8BHE0; Q8BUT6;
DT	10-OCT-2003 (Rel. 42, Created)
DT	10-OCT-2003 (Rel. 42, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Caspase recruitment domain protein 4.
GN	CARD4.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=NOD; TISSUE=Cerebellum, and Spleen;
RC	MDLLINE=22354683; PubMed12466851;
RX	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA	Nakado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogani A., Schonbach C., Gojobori T.,
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA	Blake J.A., Bratt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzieraki R.M., King B.L.,
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pestea G., Pesole G.,
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

FT	NP_BIND	202	209	ATP (POTENTIAL).
FT	REPEAT	17	42	LRR 1.
FT	REPEAT	702	725	LRR 2.
FT	REPEAT	727	750	LRR 3.
FT	REPEAT	755	778	LRR 4.
FT	REPEAT	783	806	LRR 5.
FT	REPEAT	839	862	LRR 6.
FT	REPEAT	867	890	LRR 7.
FT	REPEAT	895	918	LRR 8.
FT	REPEAT	923	946	LRR 9.
FT	VARIANT	884	884	S -> A (in strain Czech II).
SEQ	SEQUENCE	953 AA;	107739 MW;	39C63962ICEB1A58 CRC64;
 Query Match Summary Best Local Similarity    14.7%; Score 72; DB 1; Length 953; Matches    20; Conservative    26.0%; Pred.No. 20; Mismatches    17; Mismatches    38; Indels    2; Gaps    2;				
QY	8	REQIARIIVSEVVLDK-LHGQVLSGEQERYVLAEINRPSQMRFSLSQSWDRKCKDGL	66	
DB	27	REHLVTNIRNTQCIVNDLNLNGYFSAEDAEIVCACTPKDKVKRKILDVQSKGEEVSEFF	86	
QY	67	YOALKETH-PHILMELW	82	
DB	87	LYVLQQLDAYVDLRW	103	
 RESULT 10 OAS3_HUMAN				
ID	OAS3_HUMAN	STANDARD;	PRT;	1087 AA.
AC	Q9Y6K5; Q9H3P5;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	2'-5'-oligoadenylate synthetase 3 (EC 2.7.7.-) ((2-5')oligo(A) synthetase 3) (2-5A synthetase 3) (p100 OAS) (p100OAS) (P/OAKL.4). OAS3.			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=99098899; PubMed=9880533;			
RA	Rebouillat D., Hovananian A., Marie I., Hovanesian A.G.;			
RT	"The 100-KDa 2',5'-oligoadenylate synthetase catalyzing preferentially the synthesis of dimeric pppA2'p5'A molecules is composed of three homologous domains";			
RT	J. Biol. Chem. 274:1557-1565 (1999).			
RRL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21174977; PubMed=11280764;			
RA	Ito M., Shichijo S., Tsuda N., Ochi M., Harashima N., Saito N.,			
RA	Itoh K.;			
RT	"Molecular basis of T cell-mediated recognition of pancreatic cancer cells";			
RT	Cancer Res. 61:2038-2046(2001).			
RRL	[3]			
RP	SEQUENCE FROM N.A.			
RA	Muzny D., Aronson A.D., Adams C., Bunac C., Carvelli K., Chang J.,			
RA	Ganesh R., Chen J., Ding Y., Dugan S., Durbin J., Forcum J.,			
RA	Ganesh R., Garcia C., Goodman M., Gortell J.H., Haywood M.,			
RA	Hernandez J., Jackson L., Jin S., Kampal R., Karpathy S., Kovar C.,			
RA	Lau S., Leal B., Lee E., Li Y., Lichtarge O., Liu W., Losan O., Lu J.,			
RA	Ly T., Marondel I., Martinez C., Meischer S., Montgomery K., Oswal G.,			
RA	Perez I., Rashid N.D., Renault B., Rowland K., Savage L.,			
RA	Scherer S.E., Shen H., Simon M., Stoval K., Timms K.M., Todd J.,			
RA	Vo O., Williamson A., Worley K.C., Yu W., Kucherlapati R., Nelson D.,			
RA	Gibbs R.A.;			
RA	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.			
RRL	[4]			
RP	SEQUENCE OF 1-59 FROM N.A.			
RC	TISSUE=Monocytes;			
RX	MEDLINE=20564207; PubMed=11112351;			

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DE Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
DN LEUS OR SP0254.
OS Streptococcus pneumoniae.
GN Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
ON NCBI_TaxID=1313;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angluith S.S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae";
RL Science 293:498-506(2001).
CC CC -/- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
CC -/- diphosphate + L-leucyl-tRNA(Leu).
CC -/- SUBCELLULAR LOCATION: Cytoplasmic.
CC -/- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC -----
CC DN EMBL; AE007338; AAK74433.1; -.
CC DR PR; H95029; H95029.
CC TIGR; SP0254; -.
CC HAMAP; MF 00049; -.
CC InterPro; IPR002302; Leu-tRNA-synt1a.
CC InterPro; IPR002300; tRNA-synt1a.
CC InterPro; IPR001412; tRNA-synt1.
CC InterPro; IPR009008; ValRS_fleRS_edit.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00985; tRNA-SYNTHLEU.
CC TIGRFAMS; TIGR00396; leuS_bact; 1.
CC PROSITE; PS00178; AA TRNA LIGASE I; 1.
CC KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC FT SITE 41 52 "HIGH" REGION.
CC FT SITE 610 614 "KMSKS" REGION.
CC FT BINDING 613 613 ATP (BY SIMILARITY).
CC SQ SEQUENCE 833 AA; 94421 MW; 7CAA4FBSB4F99EB3 CRC64;
Query Match 14.5%; Score 71; DB 1; Length 833;
Best local similarity 25.3%; Pred. No. 22;
Matches 24; Conservative 21; Mismatches 38; Indels 12; Gaps 4;
QY 6 QYREQIARVTSTEVV-----LDKLHGQVLS--QEQYERVLAEHTPPSQMRKLFSSISQS 57
Db 659 KFLDRVYRLITSKEILANNGALDKVYNEVTKVATQIES-LKFNTAIAQLMVFVNAANK 717
QY 58 WDRKCKD--GLYQALKETHPIIMELWEKSGKKG 89
Db 718 EDKLYVDYAKGFIQLIAPFAPHLAABELMQIVAE TG 752
RESULT 12
OASB MOUSE
ID_OASB MOUSE STANDARD; PRG; 192 AA.
AC Q60856;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

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DE 2'-5'-oligoadenylate synthetase 1B (EC 2.7.7.-) ((2-5')oligo(A)  
 DE synthetase 1B) (2-5A synthetase 1B) (Fragment).  
 GN OAS1B OR OIA52.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91232962; PubMed=1709495;  
 RA Rutherford M.N., Kumar A., Nissim A., Chebath J., Williams B.R.G.;  
 RT "The murine 2-5A synthetase locus: three distinct transcripts from two  
 RT linked genes".  
 RL Nucleic Acids Res. 19:1917-1924 (1991).  
 CC -!- FUNCTION: THE 2-5A SYSTEM (THE OAS, 2-5A, AND RNASE L) MAY PLAY A  
 CC ROLE IN MEDIATING RESISTANCE TO VIRUS INFECTION, CONTROL OF CELL  
 CC GROWTH, DIFFERENTIATION, AND APOPTOSIS.  
 CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP  
 CC into ppp(A2'p5'A)n oligomers, which activate the latent RNase L  
 CC that, when activated, cleaves single-stranded RNAs.  
 CC -!- INDUCTION: By interferons.  
 CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.  
 CC  
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 CC  
 CC EMBL; X55982; CRA39455.1; -  
 DR PIR; S15661; S15661.  
 DR MGD; MGI:37430; Oas1b.  
 DR GO; GO:0003800; P:antiviral response protein activity; IDA.  
 DR InterPro; IPR006117; 2SA\_SYNTH\_2.  
 DR InterPro; IPR006116; 2SA\_SYNTH\_UB.  
 DR InterPro; IPR001201; PAP\_2SA\_CORE.  
 DR PROSITE; PS00832; 2SA\_SYNTH\_1; PARTIAL.  
 DR PROSITE; PS00833; 2SA\_SYNTH\_2; PARTIAL.  
 DR PROSITE; PS0152; 2SA\_SYNTH\_3; 1.  
 KW RNA-binding; Transferase; Nucleotidyltransferase;  
 KW Interferon induction.  
 FT NON TER 1  
 FT NON TER 192  
 FT NON TER 192 192  
 SQ SEQUENCE 192 AA; 21936 MW; 4E1C011BF9024F46 CRC64;  
 Query Match 14.3%; Score 70; DB 1; Length 192;  
 Best Local Similarity 33.3%; Pred. No. 5.4; Indels 8; Gaps 2;  
 Matches 17; Conservative 9; Mismatches 17; Indels 8; Gaps 2;  
 QY 42 NTRPSQMKFLSLSQSWDRKCKDGLYQALKETHPHLIMEL-----WEKGSK 87  
 DB 137 NCRPTKLRRLRLVTHVYQLCKEKLGDPLP---PQYALELLTLDAWEYGR 184  
 RESULT 13  
 ENP2\_CHICK STANDARD; PRT; 494 AA.  
 AC P79784;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 43, Last annotation update)  
 DE Ectonucleoside triphosphate diphosphohydrolase 2 (EC 3.6.1.3)  
 DE (NTPDase2) (Ecto-ATPase) (CD39 antigen-like 1).  
 GN ENTPD2 OR CD39L1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 68-73; 83-90; 108; 121;

RP 144-150; 154-176; 208-217; 251-259; 273-284; 337-352; 374-380;  
 RP 383-389; 448-456 AND 459-479.  
 RX TISSUE=Gizzard, and Skeletal muscle;  
 CC MEDLINE=971150869; PubMed=8995405;  
 RA Kirley T.L.;  
 RT "Complementary DNA cloning and sequencing of the chicken muscle ecto-  
 RT ATPase. Homology with the lymphoid cell activation antigen CD39.";  
 RL J. Biol. Chem. 272:1076-1081 (1997).  
 RN [2]  
 RP SEQUENCE OF 1-12 AND 154-176, AND CHARACTERIZATION.  
 RX MEDLINE=95081479; PubMed=7989647;  
 RA Stout J.G., Kirley T.L.;  
 RT "Purification and characterization of the ecto-Mg-ATPase of chicken  
 RT gizzard smooth muscle.";  
 RL J. Biochem. Biophys. Methods 29:61-75 (1994).  
 CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other  
 CC nucleotides to regulate purinergic neurotransmission. Hydrolyzes  
 CC ADP only to a marginal extent (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.  
 CC -!- COFACTOR: Requires calcium and magnesium.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- PTM: Has probably disulfide bonds.  
 CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.  
 CC  
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 CC  
 CC EMBL; U74467; AAC60071.1; -  
 DR InterPro; IPR000407; GDA1\_CD39\_NTPase.  
 DR Pfam; PF01150; GDA1\_CD39\_1.  
 DR PROSITE; PS01238; GDA1\_CD39\_NTPASE; 1.  
 KW Hydrolyase; Transmembrane; Glycoprotein; Calcium; Magnesium.  
 FT INIT MET 0 0  
 FT DOMAIN 1 3  
 FT DOMAIN 1 3  
 FT TRANSMEM 4 24  
 FT DOMAIN 25 464  
 FT TRANSMEM 465 485  
 FT DOMAIN 486 494  
 FT DOMAIN 8 13  
 FT DOMAIN 61 61  
 FT CARBOHYD 296 296  
 FT CARBOHYD 417 417  
 FT CARBOHYD 443 443  
 FT CONFLICT 11 11  
 FT CONFLICT 174 176  
 FT SEQUENCE 494 AA; 54402 MW; 1E0E0E631DA621EE CRC64;  
 Query Match 14.3%; Score 70; DB 1; Length 494;  
 Best Local Similarity 36.4%; Pred. No. 15;  
 Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;  
 QY 21 VLDKLHGQVLSCQYQYVLAENTRPSQMKFLSLSQSWDRCKD 64  
 DB 244 VLKRLSKVLAQENYQETVANPCWPTGYRKSLSLSYDPSCTE 287  
 RESULT 14  
 OAS1\_HUMAN STANDARD; PRT; 400 AA.  
 ID OAS1\_HUMAN  
 AC P00973; P04820; F29080; P29081; P78485; P78486; Q16700; Q16701;  
 AC Q96J61;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE 2'-5'-oligoadenylate synthetase 1 (EC 2.7.7.-) ((2-5')oligo(A)  
 DE synthetase 1) (2-5A synthetase 1) (p46/p42 OAS) (E18/E16).  
 DE OAS1 OR OIAS.  
 GN Homo sapiens (Human).  
 OS



OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS P41 AND P46).  
 RX MEDLINE=86081732; PubMed=2416561;  
 RA Benesh P., Moriy Y., Revel M., Chebath J.;  
 RT "Structure of two forms of the interferon-induced (2'-5') oligo A  
 RT synthetase of human cells based on cDNAs and gene sequences.";  
 RL EMBO J. 4:2249-2256(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM P41).  
 RX MEDLINE=86223945; PubMed=3754863;  
 RA Shiojiri S., Fukunaga R., Ichii Y., Sokawa Y.;  
 RT "Structure and expression of a cloned cDNA for human (2'-  
 RT 5') oligoadenylate synthetase.";  
 RL J. Biochem. 99:1455-1464(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM P41).  
 RX MEDLINE=86108911; PubMed=3753689;  
 RA Wathel M.G., Moutschen S., Cravador A., Dewit L., Defilippi P.,  
 RA Huez G.A., Content J.;  
 RT "Full-length sequence and expression of the 42 kDa 2-5A synthetase  
 RT induced by human interferon.";  
 RL FEBS Lett. 196:113-120(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS P48 AND P41).  
 RX MEDLINE=91332052; PubMed=1651324;  
 RA Ghosh S.K., Kusari J., Bandyopadhyay S.K., Samanta H., Kumar R.,  
 RA Sen G.C.;  
 RT "Cloning, sequencing, and expression of two murine  
 RT 2'-5'-oligoadenylate synthetases. Structure-function relationships.";  
 RL J. Biol. Chem. 266:15293-15299(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Muzny D., Aronson A.D., Adams C., Bunac C., Carvelli K., Chang J.,  
 RA Chacko J., Chen J., Ding Y., Dugan S., Durbin J., Forcum J.,  
 RA Ganesh R., Garcia C., Goodman M., Gortell J.H., Haywood M.,  
 RA Hernandez J., Jackson L., Jin S., Kampal R., Karpachy S., Kovar C.,  
 RA Lau S., Leal B., Lee E., Li Y., Lichtarge O., Liu W., Logan O., Lu J.,  
 RA Ly T., Marondel I., Martinez C., Merscher S., Montgomery K., Oswal G.,  
 RA Perez L., Rashid N.D., Renault B., Rowland K., Savage L.,  
 RA Scherer S.E., Shen H., Simon M., Stovall K., Timms K.M., Todd J.,  
 RA Vo Q., Williamson A., Worley K.C., Yu W., Kucherlapati R., Nelson D.,  
 RA Gibbs R.A.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM P41).  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshitoki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.Z., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP SEQUENCE OF 255-364 FROM N.A. (ISOFORM P41).  
 RX MEDLINE=83273721; PubMed=6348777;

RA Merlin G., Chebath J., Benesh P., Metz R., Revel M.;  
 RT "Molecular cloning and sequence of partial cDNA for  
 RT interferon-induced (2'-5')oligo(A) synthetase mRNA from human  
 RT cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4904-4908(1983).  
 RN [8]  
 RP SEQUENCE OF 231-400 FROM N.A. (ISOFORM P41), AND INDUCTION.  
 RX TISSUE=Lymphoblast;  
 RX MEDLINE=85284966; PubMed=2411547;  
 RA Saunders M.E., Gewirt D.R., Fugwell M.E., McMahon M.,  
 RA Williams B.R.G.;  
 RT "Human 2-5A synthetase: characterization of a novel cDNA and  
 RT corresponding gene structure.";  
 RL EMBO J. 4:1761-1768(1985).  
 RN [9]  
 RP SEQUENCE OF 1-28 FROM N.A.  
 RX MEDLINE=88082760; PubMed=3121313;  
 RA Wathel M.G., Claus I.M., Nols C.B., Content J., Huez G.A.;  
 RT "New inducers revealed by the promoter sequence analysis of two  
 RT interferon-activated human genes.";  
 RL Eur. J. Biochem. 169:313-321(1987).  
 RN [10]  
 RP SEQUENCE OF 1-27 FROM N.A.  
 RX TISSUE=Liver;  
 RX MEDLINE=88142842; PubMed=2830497;  
 RA Benesh P., Vigneron M., Perez D., Revel M., Chebath J.;  
 RT "Interferon-responsive regulatory elements in the promoter of the  
 RT human 2'-5'-oligo(A) synthetase gene.";  
 RL Mol. Cell. Biol. 7:4498-4504(1987).  
 RN [11]  
 RP SEQUENCE OF 1-27 FROM N.A.  
 RX TISSUE=Liver;  
 RX MEDLINE=88283644; PubMed=2456211;  
 RA Rutherford M.N., Hannigan G.E., Williams B.R.G.;  
 RT "Interferon-induced binding of nuclear factors to promoter elements  
 RT of the 2-5A synthetase gene.";  
 RL EMBO J. 7:751-759(1988).  
 RN [12]  
 RP MUTAGENESIS OF CVS-331; PHE-332 AND LYS-333.  
 RX MEDLINE=98070528; PubMed=9407111;  
 RA Ghosh A., Sarkar S.N., Guo W., Bandyopadhyay S., Sen G.C.;  
 RT "Enzymatic activity of 2'-5'-oligoadenylate synthetase is impaired by  
 RT specific mutations that affect oligomerization of the protein.";  
 RL J. Biol. Chem. 272:33220-33226(1997).  
 RN [13]  
 RP MUTAGENESIS OF ASP-75 AND ASP-77.  
 RX MEDLINE=99395121; PubMed=10464285;  
 RA Sarkar S.N., Ghosh A., Wang H.W., Sung S.S., Sen G.C.;  
 RT "The nature of the catalytic domain of 2'-5'-oligoadenylate  
 RT synthetases.";  
 RL J. Biol. Chem. 274:25535-25542(1999).  
 CC -!- FUNCTION: MAY PLAY A ROLE IN MEDIATING RESISTANCE TO VIRUS  
 CC INFECTION, CONTROL OF CELL GROWTH, DIFFERENTIATION, AND APOPTOSIS.  
 CC -!- CATALYTIC ACTIVITY: Binds double-stranded RNA and polymerizes ATP  
 CC into ppp(A2'p5'A)n oligomers, which activate the latent RNase L  
 CC that, when activated, cleaves single-stranded RNAs.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH DIFFERENT SUBCELLULAR  
 CC FRACTIONS SUCH AS MITOCHONDRIAL, NUCLEAR, AND ROUGH/SMOOTH  
 CC MICROSMAL FRACTIONS.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Name=p46; Synonyms=46 kDa, E18;  
 CC IsoId=P00973-1; Sequence=Displayed;  
 CC Name=p41; Synonyms=41 kDa, E16, 3-9;  
 CC IsoId=P00973-2; Sequence=VSP\_003738, VSP\_003739;  
 CC Name=p48; Synonyms=9-2;  
 CC IsoId=P00973-3; Sequence=VSP\_003740;  
 CC -!- INDUCTION: By interferons.  
 CC -!- SIMILARITY: Belongs to the 2-5A synthetase family.  
 CC -!- CAUTION: Ref.8 sequence differs from that shown due to a  
 CC frameshift in position 400.  
 CC -!- CAUTION: Ref.4 sequence was originally thought to originate from



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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:50:22 ; Search time 13.7349 Seconds  
(without alignments)  
665.325 Million cell updates/sec

Title: US-09-996-617-2\_COPY\_1335\_1429  
Perfect score: 490  
Sequence: 1 LHFVDQVREQLIARVTSVEV.....HLIMELWEKSKKGLPLSS 95

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: Pir1: \*  
2: Pir2: \*  
3: Pir3: \*  
4: Pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	490	100.0	1192	T17255	hypothetical prote
2	75	15.3	482	AB2515	hypothetical prote
3	73.5	15.0	584	D81265	hypothetical prote
4	73.5	15.0	1260	GNLR11	retrovirus-related
5	73	14.9	383	SYM502	(2'-5')oligo(A) sy
6	71	14.5	137	C71005	hypothetical prote
7	71	14.5	833	H95029	leucyl-tRNA synth
8	70	14.3	192	S15661	(2'-5')oligo(A) sy
9	70	14.3	691	D90592	hypothetical prote
10	70	14.3	1269	F84730	probable myosin he
11	69.5	14.2	384	SYHU16	(2'-5')oligo(A) sy
12	69.5	14.2	400	SYHU18	(2'-5')oligo(A) sy
13	69.5	14.2	414	SYM503	(2'-5')oligo(A) sy
14	69.5	14.2	459	A22842	(2'-5')oligo(A) sy
15	69.5	14.2	609	A43906	nuclear phosphop
16	69	14.1	833	C97901	leucine-tRNA ligas
17	69	14.1	871	C72238	preproteine translo
18	68	13.9	1034	T30574	beta-galactosidase
19	67.5	13.8	152	F70487	conserved hypothet
20	67.5	13.8	204	MNN235	nonstructural prot
21	67.5	13.8	204	MNN283	nonstructural prot
22	67.5	13.8	344	B70136	flagellar motor sw
23	67.5	13.8	527	A82431	sensor protein Unp
24	66.5	13.6	468	S21172	glutamate-tRNA lig
25	66	13.5	412	C88923	protein W03F9.1 [l
26	66	13.5	541	T48836	hypothetical prote
27	66	13.5	706	D82160	hypothetical prote
28	66	13.5	768	T27855	hypothetical prote
29	66	13.5	804	B89961	leucyl-tRNA synth

30	55.5	13.4	279	2	C86774	transposase of IS9
31	55.5	13.4	279	2	C86836	transposase of IS9
32	55.5	13.4	279	2	H86780	transposase of IS9
33	55.5	13.4	322	2	A69963	hypothetical prote
34	55.5	13.4	374	2	G83711	hypothetical prote
35	55.5	13.4	374	2	T07033	transcription fact
36	55.5	13.4	954	2	H71427	hypothetical prote
37	55.5	13.4	1039	2	S18199	myosin heavy chain
38	65	13.3	308	2	D85879	hypothetical prote
39	65	13.3	308	2	B91035	hypothetical prote
40	65	13.3	358	2	S31407	(2'-5')oligo(A) sy
41	65	13.3	791	2	C95335	hypothetical prote
42	64.5	13.2	190	2	S23712	interferon alpha-I
43	64.5	13.2	430	2	A40559	long-chain-acyl-Co
44	64.5	13.2	439	2	D86440	unknown protein [i
45	64.5	13.2	524	2	D82285	GGDEF family prote

ALIGNMENTS

RESULT 1

T17255  
hypothetical protein DKFZp586O1822.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T17255  
R:Kohrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A:Reference number: Z18722  
A:Accession: T17255  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1192 <KOE>  
A:Cross-references: ENBL:AL117470  
A:Experimental source: adult uterus; clone DKFZp586O1822  
C:Genetics:  
A>Note: DKFZp586O1822.1

Query Match 100.0%; Score 490; DB 2; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 9.5e-41;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LHFVDQVREQLIARVTSVEVLDKLHGQVLSQEQYERVLAEITRPSQMRKLFSLSQSWDR	60
DB	1098	LHFVDQVREQLIARVTSVEVLDKLHGQVLSQEQYERVLAEITRPSQMRKLFSLSQSWDR	1157
QY	61	KCKGLYQALKETHPHLIMELWEKSKKGLPLSS	95
DB	1158	KCKGLYQALKETHPHLIMELWEKSKKGLPLSS	1192

RESULT 2

AB2515  
hypothetical protein alr7298 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a  
C:Species: Nostoc sp. PCC 7120  
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AB2515  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Makazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AB2515  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-482 <KUT>  
A:Cross-references: GB:BA000020; PIDN:BA078382.1; PID:q17135836; GSPDB:GN00180  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr7298  
A:Genome: plasmid

Query Match 15.3%; Score 75; DB 2; Length 482;  
Best Local Similarity 24.1%; Pred. No. 8.8;  
Matches 21; Conservative 21; Mismatches 35; Indels 10; Gaps 3;

QY 15 VTSVEVVLDKLGQVLSQEQQYERVLAEINTRPSQWRKLFSLSQSWDRCKDGLYOALKETH 74  
DB :  
258 ITGINAELEKLNTRSKOLEQ--NNLAADNTENNIOIQELQAIAEWEKEVADN--STTKSSH 314

QY 75 PHIMEL-----WEKGSKGGLPLPS 94  
DB :  
315 AGCIVETATLGOYLSPGNRLGTLOIS 341

RESULT 3  
D81265  
hypothetical protein Cj1679 [imported] - Campylobacter jejuni (strain NCTC 11168)  
C:Species: Campylobacter jejuni  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C:Accession: D81265  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Varvliet, A.; Whitehead, S.; Barrett, T.  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervirulence  
A:Reference number: AB1250; PMID:20150912; PMID:10688204  
A:Accession: D81265  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-584 <PAR>  
A:Cross-references: GB:AL139079; GB:AL111168; MID:g6968971; PIDN:CAB73666.1; PID:g6969099  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: Cj1679

Query Match 15.0%; Score 73.5; DB 2; Length 584;  
Best Local Similarity 26.5%; Pred. No. 16;  
Matches 26; Conservative 23; Mismatches 30; Indels 19; Gaps 6;

QY 2 HF-----VDQREGLIARVTSEVVL---DKLHGQV----LSOEQYERVLAENTRSQ---MR 49  
DB :  
159 HFMQDLIDKLQGIIAQBNLNLVKLEDRLHKTENLTISKIEDFLTHQLPQKAYLLF 218

QY 50 KLFSLSQSWDRCKDGLYOALKETHPHLMELWEKSGK 87  
DB :  
219 KLFRI SDSLE-----LFQSLEQANH-HAQFWQNYAK 249

RESULT 4  
GNLR1  
retrovirus-related reverse transcriptase pseudogene - slow loris  
C:Species: Nycticebus coucang (slow loris)  
C:Date: 31-Mar-1988 #sequence\_revision 04-Jan-1996 #text\_change 14-May-1999  
C:Accession: B25313  
R:Hattori, M.; Kunara, S.; Takenaka, O.; Sakaki, Y.  
Nature 321, 625-628, 1986  
A:Title: L1 family of repetitive DNA sequences in primates may be derived from a sequence related to the ERV1 provirus  
A:Reference number: A93381; PMID:86230917; PMID:2423883  
A:Accession: B25313  
A>Status: conceptual translation of pseudogene  
A:Molecule type: DNA  
A:Residues: 1-1260 <HAT>  
A>Note: this sequence was constructed from an alignment of six sequences, determined by BLAST search against Genbank database  
C:Keywords: reverse transcriptase; pseudogene

Query Match 15.0%; Score 73.5; DB 4; Length 1260;  
Best Local Similarity 23.0%; Pred. No. 38;  
Matches 23; Conservative 24; Mismatches 38; Indels 15; Gaps 3;

QY 4 VDQYRQLTIA----RTSVTEVVDKLHGQVLSOEQYERVLAENTRSQWRKLFSLSQSWD 59  
DB :  
410 LNEYKKLYSHKYENLUKDQYLEACHLPRLSOKVEML-----NRPISSSETASTQNLP 465

QY 60 RKCKDG-----LYQALKETHPHLMELWEKSGKGLFP 92

```

Db      466 KKKSPGPGDFTSEFYQTFKEELVYPILLNLNFQNIKEGILP 50S
        :| | | | | | | | | | | | | | | | | | | | | |
RESULT 5
SYM502
(2'-5')oligo(A) synthetase (EC 2.7.7.-) 2 - mouse
N;Alternate names: 2'-5'-oligoadenylate synthetase 2
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Sep-1998
C;Accession: A39417
R;Ghosh, S.K.; Kusari, J.; Bandyopadhyay, S.K.; Samanta, H.; Kumar, R.; Sen, G.C.
J. Biol. Chem. 266, 15293-15299, 1991
A;Title: Cloning, sequencing, and expression of two murine 2'-5'-oligoadenylate synthetase genes from rat and mouse
A;Reference number: A39417; MUID:91332052; PMID:1651324
A;Accession: A39417
A;Molecule type: mRNA
A;Residues: 1-363 <GHO>
A;Cross-references: GB:M3849
A;Note: the authors translated the codon TTG for residue 259 as Arg
C;Comment: This enzyme, one of those induced by interferons, binds double-stranded RNA
A;Superfamily: oligo(A) synthetase
C;Keywords: nucleotidylyltransferase

Query Match          14.9%; Score 73; DB 1; Length 363;
Best Local Similarity 25.3%; Pred. NO. 9.9;
Matches 24; Conservative 14; Mismatches 25; Indels 32; Gaps 4;

QY      22 LDKLHQVLSQSQ-YERVLAENT-----RPSQMRKLFSLSQSW 58
           ||:|| | | | | | | | | | | | | | | | | | | | | |
DB      155 LDGLTGSYPNQIYYKLEETDLQKEGFSTCTELQRDFLKORPKLSLRLVKH 214
           ||:|| | | | | | | | | | | | | | | | | | | | | |
QY      59 DRCKDGLYQALKETHPHLIMEL----WEKGSK 88
           ||:|| | | | | | | | | | | | | | | | | | | | | |
DB      215 YQNCK---KLGLKPQVALELLTVYAWERGSMK 245
           ||:|| | | | | | | | | | | | | | | | | | | | | |

RESULT 6
C71005
hypothetical protein PH1337 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: C71005
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekiri, M.; Onifuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, S.
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71005
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-197 <XAW>
A;Cross-references: GB:AP000006; NID:G3236133; PIDN:BAA30443.1; PID:d1031386; PID:g32577
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1337

```

## RESULT · 7

H95029  
leucyl-tRNA synthetase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C:Accession: H95029  
R:Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463196  
A:Accession: H95029  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-833 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AAK74433.1; PID:g14971724; GSPDB:GN00164; TIGR:SP4  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP0254  
C:Superfamily: leucine-tRNA ligase

Query Match 14.5%; Score 71; DB 2; Length 833;  
Best Local Similarity 25.3%; Pred. No. 42;  
Matches 24; Conservative 21; Mismatches 38; Indels 12; Gaps 4;

QY 6 QYREQIARVTSVEVV-----LDKLHGQVLS--QSYERVLAENTRPSQMRKLFSLSOS 57  
Db KPLDRVRLTISKEILAEANGALDKVYNTVAVTQIES-LKFNTAIAQLMVFVNAANK 717

QY 58 WDRCKD---GLYQALKETHPHLMELWEKSKG 89  
Db 718 EDKLYVDYAGKFLIAPPAPHLABELWQVTAETG 752

RESULT 8  
S15661  
(2'-5')oligo(A) synthetase (EC 2.7.7.-) L1 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1993 #sequence\_revision 02-Jun-1994 #text\_change 16-Jul-1999  
C:Accession: S15661; S19108  
R:Rutherford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, B.R.G.  
Nucleic Acids Res. 19, 1917-1924, 1991  
A:Title: The murine 2-5A synthetase locus: three distinct transcripts from two linked ge  
A:Reference number: S15660; MUID:91232962; PMID:1709495  
A:Accession: S15661  
A:Molecule type: mRNA  
A:Residues: 1-192 <RUT>  
A:Cross-references: EMBL:X55982  
R:Williams, B.  
Submitted to the EMBL Data Library, September 1990  
A:Reference number: S19108  
A:Accession: S19108  
A:Molecule type: mRNA  
A:Residues: 1-175, 'L', 177-192 <WIL>  
A:Cross-references: EMBL:X55982; NID:949714; PIDN:CAA39455.1; PID:g49715  
C:Superfamily: oligo(A) synthetase  
C:Keywords: nucleotidyltransferase

Query Match 14.3%; Score 70; DB 2; Length 192;  
Best Local Similarity 33.3%; Pred. No. 9.3;  
Matches 17; Conservative 9; Mismatches 17; Indels 8; Gaps 2;

QY 42 NTRPSQMRKLFSLSQSDRCKDGLYQALKETHPHLMEL-----WEKSKG 87  
Db 137 NCRPTKRLRLRLTHWYQCKEKLGDPLP---FOYALELLTVDANEYGSR 184

RESULT 9  
D90592  
hypotheical protein MYPU 6440 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
C:Species: Mycoplasma pulmonis  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 22-Jun-2003

C:Accession: D90592  
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul  
A:Reference number: A9512; MUID:21267165; PMID:11353084  
A:Accession: D90592  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-691 <KUR>  
A:Cross-references: GB:AL445566; PID:g14090059; PIDN:CAC13817.1; GSPDB:GN00153  
A:Experimental source: strain UAB CTIP  
C:Genetics:  
A:Gene: MYPU 6440  
A:Genetic code: SGC3  
C:Superfamily: pullulanase type debranching enzyme

Query Match 14.3%; Score 70; DB 2; Length 691;  
Best Local Similarity 20.8%; Pred. No. 42;  
Matches 25; Conservative 21; Mismatches 34; Indels 40; Gaps 4;

QY 1 LHFVDQYREQIARVTSVEVLDKLHGQVLSQEQYERVL-----AENT 43  
Db 274 IEFDRFIEE---AHKNGIAVIMDYVYHMTNMLNNILKDYFFRENSQILFVDDFALNT 330

QY 44 RPSQMRKL-----FSLSQSDMRCKDGLYQALKETHPHLM--ELWE 83  
Db 331 ESKMRKLIIDSLVYFVEYFKVDGFRDLSFTIDKTLNLIFFKLLKINPILHGEAWE 390

RESULT 10  
F84730  
Probable myosin heavy chain [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84730  
M.; Koo, H.; Moffat, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
euss, D.; Nierman, W.C.; Shear, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
Nature 402, 761-769, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617157  
A:Accession: F84730  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1269 <STO>  
A:Cross-references: GB:AE002093; NID:96598483; PIDN:AAC69932.2; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g32240  
A:Map position: 2

Query Match 14.3%; Score 70; DB 2; Length 1269;  
Best Local Similarity 29.2%; Pred. No. 87;  
Matches 26; Conservative 22; Mismatches 33; Indels 8; Gaps 5;

QY 8 RQLIARVTSVEVLDKLHG--QVLSQEQYERVL-AENTRPSQMRKLFSLSQSDMRCKD 64  
Db 120 KDGLLSAKEKLEET-EKXHGDLVYVQKQEKIYVEGRHSSQLKSLDGLQSHDAKKE 178

QY 65 GLYQALKETHPHLMELWEKSKGKGLPL 93  
Db 179 --LTEVKAFAFDALGIEL--ESSRKLI 203

RESULT 11  
SVHU16  
(2'-5')oligo(A) synthetase (EC 2.7.7.-), splice form El6 - human  
N:Alternate names: oligoadenylate synthetase  
C:Species: Homo sapiens (man)  
C>Date: 14-Nov-1983 #sequence\_revision 28-Dec-1987 #text\_change 21-Jul-2000  
C:Accession: A91013; J05012; A23623; A01204; A24359  
R:Benech, P.; Mory, Y.; Revel, M.; Chebath, J.  
EMBO J. 4, 2249-2256, 1985  
A:Title: Structure of two forms of the interferon-induced (2'-5') oligo A synthetase of



Wed Jul 28 15:20:52 2004

us-09-996-617-2\_copy\_1335\_1429.rpr

```
C;Genetics:
A;Gene: GDB:OIAS
A;Cross-references: GDB:119465; OMIM:164350
A;Map position: 12pter-12qter
C;Superfamily: oligo(A) synthetase
C;Keywords: alternative splicing; nucleotidyltransferase

Query Match      14.2%; Score 69.5; DB 2; Length 459;
Best Local Similarity 32.0%; Pred. No. 29;
Matches 16; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

QY 44 RPSQMRKLFSLQSQWDRKCKDGLYQALKETHPHLIMEL-----WEKGSKK 88
||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 201 RPTKLSLRIVKHWYQCK-----KKLGKLPFPQYALELLTVYAWERGSMMK 246

RESULT 15
A43906
nuclear phosphoprotein xnf7 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C;Accession: A43906; S27947
E;Reddy, B.A.; Kloc, M.; Etkin, L.
Dev. Biol. 148, 107-116, 1991.
A;Title: The cloning and characterization of a maternally expressed novel zinc finger nu
A;Reference number: A43906; MUID:92038424; PMID:1936552
A;Accession: A43906
A;Molecule type: mRNA
A;Residues: 1-609 <RED>
A;Cross-references: EMBL:M63705; NID:g214914; PID:g214915
A;Note: sequence extracted from NCBI backbone (NCBIN:64515, NCBIP:64520)
C;Genetics:
A;Gene: xnf7
C;Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C;Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F;141-190/Domain: RING finger homology <RNG>

Query Match      14.2%; Score 69.5; DB 2; Length 609;
Best Local Similarity 30.6%; Pred. No. 41;
Matches 26; Conservative 19; Mismatches 31; Indels 9; Gaps 4;

QY 1 LHFVDQYREQLIARVTSVEVVLKLGQVLSEQYERVLAEATRPQMRKLFSLQSQWDR 60
||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 261 LDAVGTVRELSAIVAPLEASL-KVTEQ-LSSQSDKIEQHNKNMSQYKE--HITSEFEK 316

QY 61 KCDGLYQALKETHPHLIMELWEKG 85
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 317 -----LHKFLREEREKLEQLKEQG 336
```

Search completed: July 28, 2004, 08:55:19  
Job time : 15.7349 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:51:17 ; Search time 16.5964 Seconds  
(without alignments)  
295.514 Million cell updates/sec

Title: US-09-996-617-2\_COPY\_1335\_1429

Perfect score: 490

Sequence: 1 LHFVDQYREQLIARTVTSVEV.....HLIMELWEKSKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pdp.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pdp.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pdp.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pdp.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTUS COMB.pdp.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	51.6	193	4	US-09-340-620A-61
2	236	48.2	195	4	US-09-340-620A-49
3	216	44.1	71	4	US-09-340-620A-58
4	209	42.7	70	4	US-09-340-620A-57
5	209	42.7	70	4	US-09-340-620A-66
6	111.5	22.8	109	4	US-09-340-620A-71
7	72	14.7	164	4	US-09-245-281-41
8	72	14.7	164	4	US-09-207-359B-41
9	72	14.7	164	4	US-09-340-620A-41
10	72	14.7	164	4	US-09-865-364-41
11	72	14.7	249	4	US-09-245-281-39
12	72	14.7	249	4	US-09-207-359B-39
13	72	14.7	249	4	US-09-340-620A-39
14	72	14.7	249	4	US-09-865-364-39
15	72	14.7	409	4	US-09-207-359B-46
16	72	14.7	409	4	US-09-865-364-46
17	72	14.7	953	4	US-09-099-041A-8
18	72	14.7	953	4	US-09-245-281-8
19	72	14.7	953	4	US-09-245-281-43
20	72	14.7	953	4	US-09-207-359B-8
21	72	14.7	953	4	US-09-207-359B-43
22	72	14.7	953	4	US-09-340-620A-8
23	72	14.7	953	4	US-09-340-620A-43
24	72	14.7	953	4	US-09-865-364-8
25	72	14.7	953	4	US-09-865-364-43
26	72	14.7	966	4	US-09-207-359B-47
27	72	14.7	966	4	US-09-865-364-47

28 71.5 14.6 400 2 US-08-436-771-11 Sequence 11, Appl  
29 71.5 14.6 400 2 US-08-434-998-11 Sequence 11, Appl  
30 71.5 14.6 400 2 US-08-487-797-11 Sequence 11, Appl  
31 71.5 14.6 400 5 PCT-US95-02058-11 Sequence 11, Appl  
32 71 14.5 100 4 US-09-099-841A-10 Sequence 10, Appl  
33 71 14.5 100 4 US-09-245-281-10 Sequence 10, Appl  
34 71 14.5 100 4 US-09-207-359B-10 Sequence 10, Appl  
35 71 14.5 100 4 US-09-340-620A-10 Sequence 10, Appl  
36 71 14.5 100 4 US-09-865-364-10 Sequence 10, Appl  
37 69.5 14.2 365 3 US-08-840-146-19 Sequence 19, Appl  
38 69.5 14.2 365 3 US-09-360-220-19 Sequence 2, Appl  
39 69 14.1 833 2 US-08-844-086-2 Sequence 2, Appl  
40 69 14.1 833 2 US-09-018-211-2 Sequence 2, Appl  
41 67.5 13.8 341 4 US-09-489-039A-12069 Sequence 12069, A  
42 67.5 13.8 389 4 US-08-973-005A-11 Sequence 11, Appl  
43 66.5 13.6 839 4 US-09-758-282B-206 Sequence 206, App  
44 66 13.5 804 1 US-08-785-428-2 Sequence 2, Appl  
45 66 13.5 804 2 US-08-956-797-2 Sequence 2, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-340-620A-61

; Sequence 61, Application US/09340620A

; Patent No. 6482933

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/340,620A

; CURRENT FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/245,281

; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: US 09/207,359

; PRIOR FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 61

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-340-620A-61

Query Match 51.6%; Score 253; DB 4; Length 193;

Best Local Similarity 61.2%; Pred. No. 3.5e-23;

Matches 49; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 2 HFVDQYREQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTPFSQMKLFSLSQSWDRK 61

Db 111 HFVDQYREQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTPFSQMKLFSLSQSWDRK 170

QY 62 CKDGLYQALKETHPLIMEL 81

Db 171 CKDGLYQALKETHPLIMEL 190

##### RESULT 2

US-09-340-620A-49

; Sequence 49, Application US/09340620A

; Patent No. 6482933

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/340,620A

; CURRENT FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/245,281

```

; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 195
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-340-620A-49

```

Query Match 48.2%; Score 236; DB 4; Length 195;  
Best Local Similarity 56.8%; Pred. NO. 4.3e-21;  
Matches 46; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

```

RESULT 3
US-09-340-620A-58
; Sequence 58, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/059,
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FASTSEQ for Windows Version
; SEQ ID NO 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-58

```

```

Query Match      44.1%; Score 216; DB 4; Length 71;
Best Local Similarity 61.4%; Pred.No.3.2e-19;
Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY .1 LHFVDVDEQIARIATSVTVVVDLKHQVLDSQYERVLAEINTRPSQMRKLFSLQSQRDR 60
DB 2 LHFIDQEAALIARTVTVVWLLDALYKGLTDSQYAVRAEPTNPSQMRKLFSETPAWN 61

QY 61 KCKDGLYQAL 70
DB 62 TCKDILLQAL 71

```

RESULT 4  
US-09-340-620A-57  
; Sequence 57, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John

```

? TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
?
? FILE REFERENCE: 07334-124001
?
? CURRENT APPLICATION NUMBER: US/09/340,620A
?
? CURRENT FILING DATE: 1999-06-28
?
? PRIOR APPLICATION NUMBER: US 09/245,281
?
? PRIOR FILING DATE: 1999-02-05
?
? PRIOR APPLICATION NUMBER: US 09/207,359
?
? PRIOR FILING DATE: 1998-12-08
?
? PRIOR APPLICATION NUMBER: US 09/099,041
?
? PRIOR FILING DATE: 1998-06-17
?
? PRIOR APPLICATION NUMBER: US 09/019,942
?
? PRIOR FILING DATE: 1998-02-06
?
? NUMBER OF SEQ ID NOS: 71
?
? SOFTWARE: FastSEQ for Windows Version 4.0
?
? SEQ ID NO 57
?
? LENGTH: 70
?
? TYPE: PRT
?
? ORGANISM: Mus musculus
?
? US-09-340-620A-57

```

```

Query Match      42.7%; Score 209; DB 4; Length 70;
Best Local Similarity 60.9%; Pred.No. 2.3e-18;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY  2 HFVDQYRQLIARTVSEVVLDKLHGQVLSQEQYERVLAEATRPQMKRLFSLSQSWDRK 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  2 HFVDQRLIARIATVEVDGLDHLGSVLTGEQYQAVRAETTSQDKMKRLFSFVPSMNL 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY  62 CKDGLYQAL 70
    ||| ||| ||| |||
Db  62 CKDSLQAL 70
    ||| ||| ||| |||

```

```

RESULT 5
US-09-340-620A-66
; Sequence 66, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-340-620A-66

```

```

Query Match      42.7%; Score 209; DB 4; Length 70;
Best Local Similarity 60.9%; Pred. No. 2.3e-18;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY      2 HFVDQYEQLIARVTSVEVVDKLHQVLVSQCYQERYVLAENTRPSQMKRKLFSLSQSWDRK 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 HFVDQHQALIAARVTEYDGVLDALHGSVLTGQYQAVRAETTSQDKMKRKLFSFVPSWNL 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      62 CKDGLYQAL 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62 CKDSLQAL 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

## RESULT 6

```
US-09-340-620A-71
; Sequence 71, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Consensus sequence
; NAME/KEY: VARIANT
; LOCATION: (1)...(109)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-340-620A-71
Query Match 22.8%; Score 111.5; DB 4; Length 109;
Best Local Similarity 42.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 15; Mismatches 25; Indels 7; Gaps 4;
QY 4 VDQVREQLIARVTS--VEVVLDKLHGQ-VLSQEQYERVLAEINTPQMRKLFSLQS--WD 59
DB 11 IDGRXALLARVTDPPXDSLIDALLSRDLISEEDYEAETTXLSKVRKILLVQSKGE 70
QY 60 RKCK---DGLYQALKETHPHL 77
DB 71 ETCKXFLKCLQALKDSAAVL 91
US-09-245-281-41
RESULT 7
US-09-245-281-41
; Sequence 41, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/245,281
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-41
Query Match 14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;
QY 8 REQLIARVTSVEVVDLK-LHGQVLSQEQYERVLAEINTPQMRKLFSLQSQWDRCKD-- 64
```

```
US-09-340-620A-41
RESULT 8
US-09-340-620A-41
; Sequence 41, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-41
Query Match 14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;
QY 8 REQLIARVTSVEVVDLK-LHGQVLSQEQYERVLAEINTPQMRKLFSLQSQWDRCKD-- 64
DB 27 RELVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDQVKRILDLVQSKGEVSEFF 86
QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
DB 87 LYLQQLADAYVDLRPWLLEIGFSPSLTQS 117
US-09-340-620A-41
RESULT 9
US-09-340-620A-41
; Sequence 41, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-41
Query Match 14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;
QY 8 REQLIARVTSVEVVDLK-LHGQVLSQEQYERVLAEINTPQMRKLFSLQSQWDRCKD-- 64
DB 27 RELVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDQVKRILDLVQSKGEVSEFF 86
QY 65 -GLYQALKETHPHLIMELWEKSKKGLPLS 94
DB 87 LYLQQLADAYVDLRPWLLEIGFSPSLTQS 117
```

```
QY      8 REQLIARVTSVEVWLDK-LHGQVLSQEQYERVLAEINTPQSMRKLFSLSQSWDRKCKD-- 64
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDVKRKILDLVQSKGEVSEFF 86
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
QY      65 -GLYQALKETHPHLMELWEKSKGLPLS 94
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      87 LYLQQLADAVVDLRPWLLEIGFSPSLTQS 117
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :

RESULT 10
US-09-865-364-41
; Sequence 41, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-364-41

Query Match      14.7%; Score 72; DB 4; Length 164;
Best Local Similarity 29.7%; Pred. No. 0.42;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY      8 REQLIARVTSVEVWLDK-LHGQVLSQEQYERVLAEINTPQSMRKLFSLSQSWDRKCKD-- 64
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDVKRKILDLVQSKGEVSEFF 86
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
QY      65 -GLYQALKETHPHLMELWEKSKGLPLS 94
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      87 LYLQQLADAVVDLRPWLLEIGFSPSLTQS 117
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :

RESULT 11
US-09-245-281-39
; Sequence 39, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US/09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US/09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US/09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-39
```

```
Query Match      14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY      8 REQLIARVTSVEVWLDK-LHGQVLSQEQYERVLAEINTPQSMRKLFSLSQSWDRKCKD-- 64
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDVKRKILDLVQSKGEVSEFF 86
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
QY      65 -GLYQALKETHPHLMELWEKSKGLPLS 94
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      87 LYLQQLADAVVDLRPWLLEIGFSPSLTQS 117
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :

RESULT 12
US-09-207-359B-39
; Sequence 39, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-39

Query Match      14.7%; Score 72; DB 4; Length 249;
Best Local Similarity 29.7%; Pred. No. 0.72;
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY      8 REQLIARVTSVEVWLDK-LHGQVLSQEQYERVLAEINTPQSMRKLFSLSQSWDRKCKD-- 64
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACTQPDVKRKILDLVQSKGEVSEFF 86
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
QY      65 -GLYQALKETHPHLMELWEKSKGLPLS 94
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :
Db      87 LYLQQLADAVVDLRPWLLEIGFSPSLTQS 117
      |||: : : : :|||: : : : :|||: : : : :|||: : : : :|||: : : : :

RESULT 13
US-09-340-620A-39
; Sequence 39, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-340-620A-39

Query Match 14.7%; Score 72; DB 4; Length 249;  
Best Local Similarity 29.7%; Pred. No. 0.72;  
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;  
QY 8 REQLIARVTSVEVVDK-LHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDRKCKD-- 64  
DB 27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACPTQPKVKRILDVQSKGEEVSEFF 86  
QY 65 -GLYQALKETHPHILMELWEKSGKGLPLS 94  
DB 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117

RESULT 14

US-09-865-364-39

Sequence 39, Application US/09865364

Patent No. 8613521

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-112001

CURRENT APPLICATION NUMBER: US/09/865,364

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 09/207,359

PRIOR FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 39

LENGTH: 249

TYPE: PRT

ORGANISM: Homo sapiens

US-09-865-364-39

Query Match 14.7%; Score 72; DB 4; Length 249;  
Best Local Similarity 29.7%; Pred. No. 0.72;  
Matches 27; Conservative 14; Mismatches 46; Indels 4; Gaps 2;

QY 8 REQLIARVTSVEVVDK-LHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDRKCKD-- 64  
DB 27 RELLVTHIRNTQCLVDNLLKNDYFSAEDAIVCACPTQPKVKRILDVQSKGEEVSEFF 86

QY 65 -GLYQALKETHPHILMELWEKSGKGLPLS 94

DB 87 LYLQQLADAYVDLRPWLEIGFSPSLTQS 117

RESULT 15

US-09-207-359B-46

Sequence 46, Application US/09207359B

Patent No. 6469140

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

FILE REFERENCE: 07334-112001

CURRENT APPLICATION NUMBER: US/09/207,359B

CURRENT FILING DATE: 1998-12-08

PRIOR APPLICATION NUMBER: US 09/099,041

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: US 09/019,942

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 46

LENGTH: 409

TYPE: PRT



Result No.	§			Description	
	Score	Match	Length	ID	
1	490	100.0	1399	9	US-09-388-221-4
2	490	100.0	1429	9	US-09-996-617-2
3	490	100.0	1429	9	US-09-931-071-2
4	490	100.0	1429	12	US-10-029-347-3
5	490	100.0	1429	12	US-10-029-347-26
6	490	100.0	1429	14	US-10-038-392-11
7	490	100.0	1429	14	US-10-028-374-3
8	490	100.0	1429	14	US-10-028-374-15
9	490	100.0	1429	14	US-10-183-770-3
10	490	100.0	1429	14	US-10-183-770-15
11	490	100.0	1443	9	US-09-388-221-6
12	490	100.0	1473	9	US-09-388-221-2
13	490	100.0	1473	12	US-10-182-822A-8
14	427	87.1	88	9	US-09-841-739-15
15	427	87.1	88	14	US-10-449-315-15

; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-340001  
; CURRENT APPLICATION NUMBER: US/09/996.617  
; CURRENT FILING DATE: 2001-11-27  
; PRIOR APPLICATION NUMBER: 09/931,071  
; PRIOR FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/428,252  
; PRIOR FILING DATE: 1999-10-27  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-617-2

Query Match 100.0%; Score 490; DB 9; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 7.5e-46;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 60  
DB 1335 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 1394  
QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95  
DB 1395 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1429

RESULT 3  
US-09-931-071-2  
; Sequence 2, Application US/09931071  
; Patent No. US20020128219A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Alhemri, Enad S.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-335001  
; CURRENT APPLICATION NUMBER: US/09/931,071  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/428,252  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-931-071-2

Query Match 100.0%; Score 490; DB 9; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 7.5e-46;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 60  
DB 1335 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 1394  
QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95  
DB 1395 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1429

RESULT 4  
US-10-029-347-3  
; Sequence 3, Application US/10029347  
; Publication No. US20030017562A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED

; TITLE OF INVENTION: PREDOMINATELY IN SMALL INTESTINE, HLRRS11  
; FILE REFERENCE: D0066  
; CURRENT APPLICATION NUMBER: US/10/029,347  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 1429  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-029-347-3

Query Match 100.0%; Score 490; DB 12; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 7.5e-46;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 60  
DB 1335 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 1394  
QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95  
DB 1395 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1429

RESULT 5  
US-10-029-347-26  
; Sequence 26, Application US/10029347  
; Publication No. US20030017562A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED  
; TITLE OF INVENTION: PREDOMINATELY IN SMALL INTESTINE, HLRRS11  
; FILE REFERENCE: D0066  
; CURRENT APPLICATION NUMBER: US/10/029,347  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 1429  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-029-347-26

Query Match 100.0%; Score 490; DB 12; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 7.5e-46;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 60  
DB 1335 LHFVDQYREQLIARVTSVEVVDKLGQVLSQEQYERVLAEHTRPQSRKLFSLQSQWDR 1394  
QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95  
DB 1395 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1429

RESULT 6  
US-10-028-392-11  
; Sequence 11, Application US/10028392  
; Publication No. US20030087340A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED  
; TITLE OF INVENTION: PREDOMINATELY IN NERVOUS SYSTEM TISSUES, HLRRS1  
; FILE REFERENCE: D0085.np  
; CURRENT APPLICATION NUMBER: US/10/028,392  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/259,479  
; PRIOR FILING DATE: 2001-01-03  
; PRIOR APPLICATION NUMBER: US 60/260,616  
; PRIOR FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 63



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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-374-11

Query Match      100.0%; Score 490; DB 14; Length 1429;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 60
        |||
Db      1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 1394
        |||

QY      61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
        |||
Db      1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429
        |||

RESULT 7
US-10-028-374-3
; Sequence 3, Application US/10028374
; Publication No. US20030143706A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRRBML
; FILE REFERENCE: D0067NP
; CURRENT FILING DATE: 2001-12-20
; CURRENT APPLICATION NUMBER: US/10/028,374
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/257,773
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-374-3

Query Match      100.0%; Score 490; DB 14; Length 1429;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 60
        |||
Db      1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 1394
        |||

QY      61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
        |||
Db      1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429
        |||

RESULT 8
US-10-028-374-15
; Sequence 15, Application US/10028374
; Publication No. US20030143706A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRRBML
; FILE REFERENCE: D0067NP
; CURRENT FILING DATE: 2001-12-20
; CURRENT APPLICATION NUMBER: US/10/028,374
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/257,773
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: homo sapiens
```

```
US-10-028-374-15

Query Match      100.0%; Score 490; DB 14; Length 1429;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 60
        |||
Db      1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 1394
        |||

QY      61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
        |||
Db      1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429
        |||

RESULT 9
US-10-183-770-3
; Sequence 3, Application US/10183770
; Publication No. US20030180812A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRRBML
; FILE REFERENCE: D0067A CIP
; CURRENT APPLICATION NUMBER: US/10/183,770
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/257,773
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 10/028,374
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-183-770-3

Query Match      100.0%; Score 490; DB 14; Length 1429;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 60
        |||
Db      1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAENTRPSQMRKLFSLQSQWDR 1394
        |||

QY      61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95
        |||
Db      1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429
        |||

RESULT 10
US-10-183-770-15
; Sequence 15, Application US/10183770
; Publication No. US20030180812A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE OF INVENTION: PREDOMINATELY IN BONE MARROW, HLRRBML
; FILE REFERENCE: D0067A CIP
; CURRENT APPLICATION NUMBER: US/10/183,770
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/257,773
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 10/028,374
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1429
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-183-770-15
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Query Match 100.0%; Score 490; DB 14; Length 1429;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-46;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60  
 |||||  
 DB 1335 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1394

QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95  
 |||||  
 DB 1395 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1429

RESULT 11  
 US-09-388-221-6  
 ; Sequence 6, Application US/09388221A  
 ; Publication No. US20020192643A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, John C.  
 ; TITLE OF INVENTION: No. US20020192643A1e1 Card Proteins Involved in Cell Death Regul  
 ; FILE REFERENCE: P-LJ 3650  
 ; CURRENT APPLICATION NUMBER: US/09/388,221A  
 ; CURRENT FILING DATE: 1999-09-01  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 1443  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-388-221-6

Query Match 100.0%; Score 490; DB 9; Length 1443;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-46;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60  
 |||||  
 DB 1349 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1408

QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95  
 |||||  
 DB 1409 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1443

RESULT 12  
 US-09-388-221-2  
 ; Sequence 2, Application US/09388221A  
 ; Publication No. US20020192643A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, John C.  
 ; TITLE OF INVENTION: No. US20020192643A1e1 Card Proteins Involved in Cell Death Regul  
 ; FILE REFERENCE: P-LJ 3650  
 ; CURRENT APPLICATION NUMBER: US/09/388,221A  
 ; CURRENT FILING DATE: 1999-09-01  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1473  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-388-221-2

Query Match 100.0%; Score 490; DB 9; Length 1473;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-46;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60  
 |||||  
 DB 1379 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1438

QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95  
 |||||

DB 1439 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1473

RESULT 13  
 US-10-182-822A-8  
 ; Sequence 8, Application US/10182822A  
 ; Publication No. US20030211493A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.  
 ; APPLICANT: AU-YOUNG, Janice; YUE, Henry  
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
 ; FILE REFERENCE: PI-0032 USN  
 ; CURRENT APPLICATION NUMBER: US/10/182,822A  
 ; CURRENT FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: PCT/US 01/03455  
 ; PRIOR FILING DATE: 2001-01-02  
 ; PRIOR APPLICATION NUMBER: US 60/180,093  
 ; PRIOR FILING DATE: 2000-02-02  
 ; PRIOR APPLICATION NUMBER: US 60/182,045  
 ; PRIOR FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 8  
 ; LENGTH: 1473  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: 4250893CD1  
 US-10-182-822A-8

Query Match 100.0%; Score 490; DB 12; Length 1473;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-46;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60  
 |||||  
 DB 1379 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 1438

QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95  
 |||||  
 DB 1439 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1473

RESULT 14  
 US-09-841-739-15  
 ; Sequence 15, Application US/09841739  
 ; Patent No. US20020034784A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
 ; FILE REFERENCE: 07334-329001  
 ; CURRENT APPLICATION NUMBER: US/09/841,739  
 ; CURRENT FILING DATE: 2001-08-29  
 ; PRIOR APPLICATION NUMBER: US 09/697,089  
 ; PRIOR FILING DATE: 2000-10-26  
 ; PRIOR APPLICATION NUMBER: US 60/161,822  
 ; PRIOR FILING DATE: 1999-10-27  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 88  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-841-739-15

Query Match 87.1%; Score 427; DB 9; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-40;  
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 60  
 |||||  
 DB 7 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVAENTRPSQMRKLFSLSQSWDR 66

QY 61 KCKDGLYQALKETHPHILMELW 82  
Db 67 KCKDGLYQALKETHPHILMELW 88

RESULT 15  
US-10-449-315-15  
; Sequence 15, Application US/10449315  
; Publication No. US20030190679A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/10/449,315  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: US /09/841,739  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 88  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-449-315-15

Query Match 87.1%; Score 427; DB 14; Length 88;  
Best Local Similarity 100.0%; Pred. No. 2.8e-40;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVVDKLGQVLSQFQYERVLAEINTRPSOMEKLFSLQSOWDR 60  
Db 7 LHFVDQYREQLIARVTSVEVVDKLGQVLSQFQYERVLAEINTRPSOMEKLFSLQSOWDR 66

QY 61 KCKDGLYQALKETHPHILMELW 82  
Db 67 KCKDGLYQALKETHPHILMELW 88

Search completed: July 28, 2004, 09:04:14  
Job time : 47.3554 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:11 ; Search time 54.9398 Seconds  
(without alignments)  
488.572 Million cell updates/sec

Title: US-09-996-617-2\_COPY\_1335\_1429  
Perfect score: 490  
Sequence: 1 LHFVQYRQLIARVTSVEV.....HLIMELWKGKGLPLSS 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	490	100.0	1397	4	AAY72670 Human NB-
2	490	100.0	1429	4	AAB62571 Human NB-
3	490	100.0	1429	5	ABG78455 Human cas
4	490	100.0	1429	5	ABG78472 Leucine-r
5	490	100.0	1429	5	ABG77916 Human leu
6	490	100.0	1429	5	ABG7969 Human leu
7	490	100.0	1429	5	AAO17855 Pyrin dom
8	490	100.0	1429	6	ABG71631 Human cas
9	490	100.0	1429	6	ABP96889 Human cas
10	490	100.0	1429	6	ABP96888 Human NAC
11	490	100.0	1429	6	ABG71633 Human cas
12	490	100.0	1442	4	AAY72671 Human NB-
13	490	100.0	1473	4	AAE06758 Human G-P
14	490	100.0	1473	4	AAY72669 Human NB-
15	490	100.0	1473	4	AAY72711 Human NAC
16	404.5	82.6	442	3	AAB24513 Human sec
17	253	51.6	193	4	AAB20086 Mouse car
18	253	51.6	193	4	AAE00592 Mouse tar
19	253	51.6	193	5	AAU93352 Mouse cas
20	236	48.2	84	4	AAE00591 Human tar
21	236	48.2	176	4	AAE00594 Alternati
22	236	48.2	195	2	AAY48553 Human bre
23	236	48.2	195	4	AAU68525 Human nov
24	236	48.2	195	4	AAB20085 Human CAR
25	236	48.2	195	4	AAE00588 Human tar

26	236	48.2	195	5	AAU93353 Human cas
27	236	48.2	195	5	AAO17854 Pyrin dom
28	236	48.2	195	6	ABG71635 Human cas
29	236	48.2	205	4	AAAG74647 Human col
30	224	45.7	65	3	AAAB24519 Human sec
31	216	44.1	171	4	AAE00593 Rat targe
32	180.5	36.8	59	3	AAB24520 Human sec
33	127.5	26.0	158	4	AAAG74648 Human col
34	127.5	26.0	190	3	AAAB33675 Human can
35	94.5	19.3	87	6	ABB2737 Human TUC
36	94.5	19.3	230	4	AAU21812 Novel hum
37	94.5	19.3	230	7	ADC46453 Human neo
38	94.5	19.3	431	4	AAAB2572 Human CAR
39	94.5	19.3	431	4	AAAY72672 Human CAR
40	94.5	19.3	431	6	ABU03496 Angiogene
41	94.5	19.3	431	6	ABG71632 Human cas
42	94.5	19.3	431	6	ABB2736 Human TUC
43	94.5	19.3	431	6	ABG71634 Human cas
44	94.5	19.3	488	4	AAU21689 Novel hum
45	94.5	19.3	488	7	ADC46330 Human neo

ALIGNMENTS

RESULT 1  
AAV72670  
ID AAY72670 standard; protein; 1397 AA.  
XX

AC AAY72670;

XX 31-MAY-2001 (first entry)

XX Human NB-ARC and CARD containing protein (NAC) gamma isoform.

XX Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;  
caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;  
cysteine aspartyl protease; apoptosis; cytokine production;  
cysteine receptor signalling; therapy; inflammatory disorder; sepsis;  
fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 1..956  
FT Region /note= "Corresponds to 1-956 residues of human NAC beta isoform (AAY72669)"  
FT FT 957..1229  
FT Region /note= "Corresponds to 988-1260 residues of human NAC beta isoform (AAY72669)"  
FT Region 1230..1397  
FT /note= "Corresponds to 1306-1473 residues of human NAC beta isoform (AAY72669)"

XX WO200116170-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-US024152.

XX 01-SEP-1999; 99US-00388221.

XX (BURN-) BUENHAM INST.

XX Reed JC;

XX WPI; 2001-183258/18.

XX N-PSDB; AAD02761.

XX Novel nucleic acid encoding NB-ARC and caspase associated recruitment domains, used to produce polypeptides for screening for modulators of apoptosis.

XX

PS Claim 15; Page 143-148; 184pp; English.

XX The present sequence is a human NB-ARC and CARD containing protein (NAC)

CC gamma isoform. NAC gamma isoform represents the NAC splice variant in

CC which both the splice regions are absent in the translated polypeptide.

CC NAC protein comprises a nucleotide binding (NB) domain (also referred as

CC NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-

CC Barrel-like domain. The caspases, cysteine aspartyl proteases, are

CC principal effectors of apoptosis. CARD containing NAC proteins are used

CC for screening modulators that modulates apoptosis, cytokine production,

CC cytokine receptor signaling and other cellular processes. NAC can act as

CC an immunogen for the production of polyclonal and monoclonal antibodies.

CC It can also be used to diagnose and treat inflammatory disorders such as

CC sepsis, fibrosis and arthritis and cancer pathologies such as

CC adenocarcinomas and leukaemias

XX Sequence 1397 AA;

SQ

Query Match 100.0%; Score 490; DB 4; Length 1397;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTSVSEVVDKLGQVLSQEQYERVLAEPTPSQMRKLFSLQSQWDR 60

Db 1303 LHFVDQYREQLIARTSVSEVVDKLGQVLSQEQYERVLAEPTPSQMRKLFSLQSQWDR 1362

QY 61 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 95

Db 1363 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 1397

RESULT 2

AAB62571

ID AAB62571 standard; protein; 1429 AA.

XX AC AAB62571;

XX

DT 23-JUN-2001 (first entry)

DE Human CARD-7 polypeptide.

XX CARD-7; CARD-8; CARD-5; caspase recruitment domain; cancer; human;

XX auto-immune disorder; anti-inflammatory; immunosuppressive; anti-allergic;

XX antibacterial; antiviral; gene therapy.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 329..645

FT Domain /note="nucleotide binding domain"

FT 333..341

FT Domain /note="kinase 1A subdomain"

FT 404..413

FT Domain /note="kinase 2 subdomain"

FT 454..463

FT Domain /note="kinase 3a subdomain"

FT 615..622

FT Domain /note="motif 2 domain"

FT 807..834

FT Domain /note="leucine-rich domain"

FT 836..863

FT Domain /note="leucine-rich domain"

FT 864..891

FT Domain /note="leucine-rich domain"

FT 893..920

FT Domain /note="leucine-rich domain"

FT 921..948

FT Domain /note="leucine-rich domain"

FT 950..976

FT Domain /note="leucine-rich domain"

XX WO200130813-A1.

XX

PD 03-MAY-2001.

XX

PF 27-OCT-2000; 2000WO-US029796.

XX

PR 27-OCT-1999; 99US-00428252.

XX (MILL-) MILLENNIUM PHARM INC.

PA Bertin J;

XX

PI WPI; 2001-343340/36.

XX

DR N-PSDB; AAF83651.

XX

DR

XX

PT Identifying a modulator of interaction between caspase recruitment domain

PT (CARD)-7 and CARD-5, for treating autoimmune disorders, comprises

PT measuring the binding of CARD-7 and CARD-5 in the presence of the

PT compound.

XX

PS Disclosure; Fig 1A-D; 80pp; English.

XX

XX The invention relates to identifying compounds, that modulate interaction

CC between caspase recruitment domain (CARD)-7 and CARD-5. The method

CC involves measuring the binding of CARD-7 and CARD-5 in the presence of

CC the compound (an increase in the binding of CARD-7 to CARD-5 in the

CC presence of the compound compared to the binding in the absence of the

CC compound indicates that the compound is a modulator of CARD-7-CARD-5

CC interaction). Modulators of CARD-7 and CARD-8 expression or activity can

CC be used to treat or diagnose disorders such as cancers, bacterial or

CC viral infections, autoimmune disorders (systemic lupus erythematosus,

CC immune-mediated glomerulonephritis or arthritis), inflammatory disorders,

CC organ-specific autoimmunity including multiple sclerosis, Hashimoto's

CC thyroiditis, or Grave's disease, psoriasis, graft rejection, allergies.

CC CARD-7 and CARD-8 are useful as modulating agents in regulating a variety

CC of cellular processes including cell growth and cell death. The present

CC sequence represents the human CARD-7, an intracellular protein

XX

SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 4; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTSVSEVVDKLGQVLSQEQYERVLAEPTPSQMRKLFSLQSQWDR 60

Db 1335 LHFVDQYREQLIARTSVSEVVDKLGQVLSQEQYERVLAEPTPSQMRKLFSLQSQWDR 1394

QY 61 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 95

Db 1395 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 1429

RESULT 3

ABG78455

ID ABG78455 standard; protein; 1429 AA.

XX AC ABG78455;

XX

DT 15-NOV-2002 (first entry)

DE Human caspase recruitment protein 7 protein.

XX

XX Human; human leucine-rich repeat small intestine I; HLRRS11; asthma;

XX proliferative disorder; gastrointestinal disorder; renal disorder;

XX neural disorder; reproductive disorder; calcium regulation; apoptosis;

XX immune system; anaemia; human immune deficiency virus; HIV; cancer;

XX blood coagulation disorder; autoimmune disorder; allergic reaction;

XX inflammatory condition; cardiovascular disorder; ischaemia;

XX neurological disorder; infectious disease; cytokine production;

XX expressed sequence tag; EST.

OS Homo sapiens.

XX

PN WO200261086-A2.

XX

XX 08-AUG-2002.  
 PD  
 XX 20-DEC-2001; 2001WO-US049739.  
 PF  
 XX 22-DEC-2000; 2000US-0257774P.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX Feder J, Ramanathan C, Mintier G;  
 PI  
 XX WPI; 2002-619252/66.  
 DR  
 XX New isolated nucleic acid molecules encoding HLRS11 polypeptides, or  
 XX their fragments and homologues, useful for preventing, treating and  
 PT ameliorating medical conditions, e.g. proliferative, gastrointestinal, or  
 PT renal disorders.  
 PT  
 XX  
 PS Disclosure; Fig 2; 336pp; English.  
 XX  
 XX The invention relates to isolated nucleic acid molecules (I) encoding  
 CC human leucine-rich repeat small intestine I (HLRS11) polypeptides. The  
 CC nucleic acid molecules and polypeptides are useful for preventing,  
 CC treating and ameliorating medical conditions, such as proliferative,  
 CC gastrointestinal, renal, neural, or reproductive disorders; or disorders  
 CC related to aberrant calcium regulation or apoptosis modulation, either  
 CC directly or indirectly. They are also useful for treating, preventing  
 CC and/or diagnosing diseases, disorders and/or conditions of: immune system  
 CC by activating or inhibiting the proliferation, differentiation, or  
 CC mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia,  
 CC anaemia; immunologic deficiency syndromes, e.g. human immune deficiency  
 CC virus (HIV) infection, HTLV-BLV infection; blood coagulation disorders,  
 CC e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease,  
 CC myasthenia gravis; asthma or allergic reactions; inflammatory conditions,  
 CC e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer;  
 CC cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias,  
 CC aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's  
 CC chorea; infectious diseases, e.g. measles, mumps, pneumonia, or viral,  
 CC bacterial, and fungal infections. The HLRS11 polypeptides are useful for  
 CC modulating cytokine production, antigen presentation, or other processes  
 CC such as boosting immune responses. ABG78454-ABG78474 represent HLRS11  
 CC amino acid sequences and related amino acid sequences of the invention  
 XX  
 XX Sequence 1429 AA;  
 SQ  
 Query Match 100.0%; Score 490; DB 5; Length 1429;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTRPSQMRKLSLSQSWDR 60  
 Db 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTRPSQMRKLSLSQSWDR 1394  
 QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95  
 Db 1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429  
 RESULT 4  
 ABG78472  
 ID ABG78472 standard; protein; 1429 AA.  
 XX  
 AC ABG78472;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 XX Leucine-rich repeat (LRR) domain containing protein #2.  
 XX  
 XX Human; human leucine-rich repeat small intestine I; HLRS11; asthma;  
 XX proliferative disorder; gastrointestinal disorder; renal disorder;  
 KW neural disorder; reproductive disorder; calcium regulation; apoptosis;  
 KW immune system; anaemia; human immune deficiency virus; HIV; cancer;  
 KW blood coagulation disorder; autoimmune disorder; allergic reaction;

KW inflammatory condition; cardiovascular disorder; ischaemia;  
 KW neurological disorder; infectious disease; cytokine production;  
 KW expressed sequence tag; EST.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200261086-A2.  
 FN  
 XX 08-AUG-2002.  
 PD  
 XX 20-DEC-2001; 2001WO-US049739.  
 PF  
 XX 22-DEC-2000; 2000US-0257774P.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX Feder J, Ramanathan C, Mintier G;  
 PI  
 XX WPI; 2002-619252/66.  
 DR  
 XX New isolated nucleic acid molecules encoding HLRS11 polypeptides, or  
 PT their fragments and homologues, useful for preventing, treating and  
 PT ameliorating medical conditions, e.g. proliferative, gastrointestinal, or  
 PT renal disorders.  
 PT  
 XX  
 PS Disclosure; Page 229-233; 336pp; English.  
 XX  
 XX The invention relates to isolated nucleic acid molecules (I) encoding  
 CC human leucine-rich repeat small intestine I (HLRS11) polypeptides. The  
 CC nucleic acid molecules and polypeptides are useful for preventing,  
 CC treating and ameliorating medical conditions, such as proliferative,  
 CC gastrointestinal, renal, neural, or reproductive disorders; or disorders  
 CC related to aberrant calcium regulation or apoptosis modulation, either  
 CC directly or indirectly. They are also useful for treating, preventing  
 CC and/or diagnosing diseases, disorders and/or conditions of: immune system  
 CC by activating or inhibiting the proliferation, differentiation, or  
 CC mobilisation of immune cells; haematopoietic cells e.g. thrombocytopenia,  
 CC anaemia; immunologic deficiency syndromes, e.g. human immune deficiency  
 CC virus (HIV) infection, HTLV-BLV infection; blood coagulation disorders,  
 CC e.g. arterial thrombosis; autoimmune disorders, e.g. Addison's disease,  
 CC myasthenia gravis; asthma or allergic reactions; inflammatory conditions,  
 CC e.g. chronic prostatitis, sepsis; proliferative disorders, e.g. cancer;  
 CC cardiovascular disorders, e.g. arrhythmia, myocardial ischaemias,  
 CC aneurysms; neurological disorders, e.g. Alzheimer's disease, Huntington's  
 CC chorea; infectious diseases, e.g. measles, mumps, pneumonia, or viral,  
 CC bacterial, and fungal infections. The HLRS11 polypeptides are useful for  
 CC modulating cytokine production, antigen presentation, or other processes  
 CC such as boosting immune responses. ABG78454-ABG78474 represent HLRS11  
 CC amino acid sequences and related amino acid sequences of the invention  
 XX  
 XX Sequence 1429 AA;  
 SQ  
 Query Match 100.0%; Score 490; DB 5; Length 1429;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTRPSQMRKLSLSQSWDR 60  
 Db 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTRPSQMRKLSLSQSWDR 1394  
 QY 61 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 95  
 Db 1395 KCKDGLYQALKETHPHLIMELWEKSKKGLPLSS 1429  
 RESULT 5  
 ABB77916  
 ID ABB77916 standard; protein; 1429 AA.  
 XX  
 AC ABB77916;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX

DE Human leucine-rich repeat domain containing protein KIAA0926.  
 XX Human; leucine-rich repeat; HLRRBM1; proliferative disorder;  
 KW immune condition; apoptosis; signal transduction; autoimmune disease;  
 KW haematopoietic cell disease; graft-versus-host disease; allergy; asthma;  
 KW cardiovascular disorder; neurological disease; pheromone;  
 KW pulmonary disease; chronic obstructive pulmonary disease;  
 KW allergic rhinitis; bronchial hyperresponsiveness; reproductive disease;  
 KW haematopoietic disease; platelet disorder; Bernard-Soulier syndrome;  
 KW inflammatory disorder; systemic lupus erythematosus;  
 KW cardiovascular disease; cancer; KIAA0926.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200252011-A2.  
 XX  
 XX 04-JUL-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-US049740.  
 XX  
 XX 22-DEC-2000; 2000US-0257773P.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX Feder J, Ramanathan C, Mintier G;  
 XX WPI; 2002-566676/60.  
 DR  
 XX  
 XX New HLRRBM1 nucleic acids for preventing, treating or ameliorating e.g.  
 PT proliferative disorders, immune conditions, a disorder related to  
 PT aberrant apoptosis modulation or developmental disorders.  
 XX  
 XX Example 1; Page 362-366; 371pp; English.  
 XX  
 CC The present sequence represents a human leucine-rich repeat domain  
 CC containing protein, which was used as a probe to search for leucine-rich  
 CC repeat containing protein HLRRBM1. HLRRBM1 polypeptides and  
 CC polynucleotides are useful for preventing, treating or ameliorating a  
 CC medical condition such as a proliferative disorder, immune condition, or  
 CC a disorder related to aberrant apoptosis modulation, either directly or  
 CC indirectly, and in modulating signal transduction activity in various  
 CC cells, tissue and organisms. They are also useful for treating,  
 CC preventing, or diagnosing diseases of haematopoietic cells, autoimmune  
 CC disease, graft-versus-host disease, allergic conditions (e.g. asthma),  
 CC cardiovascular disorders, and neurological diseases, and for increasing  
 CC the organisms' ability to synthesize and/or release pheromones. The  
 CC polypeptide may also be used in treating, preventing or ameliorating  
 CC pulmonary disease (e.g. chronic obstructive pulmonary disease, allergic  
 CC rhinitis, or bronchial hyperresponsiveness), reproductive disease,  
 CC haematopoietic disease, platelet disorders (e.g. Bernard-Soulier  
 CC syndrome), non-infectious disorders (e.g. innate immunity to bacterial  
 CC pathogens, or adaptive immune response), immune and inflammatory  
 CC disorders (e.g. systemic lupus erythematosus), cardiovascular diseases  
 CC and cancers. HLRRBM1 nucleic acids may further be used in chromosome  
 CC identification or mapping, as a chromosome marker, as molecular weight  
 CC markers, as diagnostic probes, in gene therapy, in raising anti-DNA  
 CC antibodies, or as antigens for eliciting immune responses  
 XX  
 SQ Sequence 1429 AA;  
 Query Match 100.0%; Score 490; DB 5; Length 1429;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LHFVDQYREQLIARVTSVEVVDKLHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 60  
 Db 1335 LHFVDQYREQLIARVTSVEVVDKLHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 1394  
 QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95  
 Db 1395 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 1429

RESULT 6  
 ABG97969  
 ID ABG97969 standard; protein; 1429 AA.  
 XX  
 AC ABG97969;  
 XX  
 DT 07-JAN-2003 (first entry)  
 XX  
 DE Human leucine rich repeat domain containing protein #2.  
 XX  
 XX Leucine rich repeat; nervous system; human; neural disorder; apoptosis;  
 KW renal disorder; immune disorder; arthritis; asthma; AIDS;  
 KW acquired immunodeficiency syndrome; rheumatoid arthritis;  
 KW haematopoietic disorder; metabolic disorder; reproductive disorder;  
 KW pulmonary disease; cardiovascular disease; hyperproliferative disorder;  
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; developmental disorder; autoimmune disease;  
 KW Addison's disease; haemolytic anaemia; antiphospholipid syndrome;  
 KW allergic encephalomyelitis; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200274959-A2.  
 XX  
 XX 26-SEP-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-US050457.  
 XX  
 XX 03-JAN-2001; 2001US-0259479P.  
 PR  
 XX 09-JAN-2001; 2001US-0260616P.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX Ramanathan C, Feder J, Mintier G;  
 XX WPI; 2002-750554/81.  
 XX  
 XX New HLRRNSI nucleic acids and polypeptides, useful for preventing,  
 PT treating, or ameliorating e.g. renal disorder, immune, haematopoietic,  
 PT metabolic, reproductive, pulmonary, cardiovascular or autoimmune  
 PT diseases.  
 XX  
 XX Example 1; Page 392-397; 415pp; English.  
 PS  
 CC The invention describes nucleic acids encoding human leucine-rich repeat  
 CC containing proteins expressed in nervous system tissues, HLRRNSI. The  
 CC HLRRNSI polypeptide or the polynucleotide is useful for preventing,  
 CC treating, or ameliorating a neural disorder or a disorder related to  
 CC aberrant apoptosis modulation (either directly or indirectly), renal  
 CC disorder, immune disorder (e.g. arthritis, asthma, acquired  
 CC immunodeficiency syndrome (AIDS) or rheumatoid arthritis),  
 CC haematopoietic, metabolic, reproductive, pulmonary or cardiovascular  
 CC diseases, hyperproliferative disorders, neurodegenerative diseases (e.g.  
 CC Alzheimer's disease, Parkinson's disease or Huntington's disease),  
 CC developmental disorders, non-infections disorders, nervous system  
 CC diseases and/or disorders, and autoimmune diseases (e.g. Addison's  
 CC disease, haemolytic anaemia, antiphospholipid syndrome, or allergic  
 CC encephalomyelitis). The polynucleotides are also useful as chromosome  
 CC markers, for chromosome identification, gene therapy, and in identifying  
 CC organisms from minute biological samples. This is the amino acid sequence  
 CC of a leucine-rich repeat containing protein  
 XX  
 SQ Sequence 1429 AA;  
 Query Match 100.0%; Score 490; DB 5; Length 1429;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LHFVDQYREQLIARVTSVEVVDKLHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 60  
 Db 1335 LHFVDQYREQLIARVTSVEVVDKLHGQVLSQEQYERVLAEINTRPSQMRKLFSLSQSWDR 1394  
 QY 61 KCKDGLYQALKETHPHLIMELWEKSGKGLPLSS 95



[illegible]

CC etc). The present sequence represents human CARD-7

XX Sequence 1429 AA;

SQ

Query Match 100.0%; Score 490; DB 6; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQMRKLFSLSQSWDR 60

DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQMRKLFSLSQSWDR 1394

QY 61 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 95

DB 1395 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 1429

RESULT 9

ABP96889

ID ABP96889 standard; protein; 1429 AA.

XX AC ABP96889;

XX DT 16-JUN-2003 (first entry)

XX DE Human caspase recruitment domain protein 7 SEQ ID NO:12.

XX KW Human; cytostatic; neurotropic; neuroprotective; antiinflammatory;

XX KW antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;

XX KW death effector filament-forming CED4-like apoptosis protein;

XX KW neurological disease; infection; inflammation; tumour formation;

XX KW caspase recruitment domain protein 7.

XX OS Homo sapiens.

XX PN WO2003024988-A1.

XX PD 27-MAR-2003.

XX PF 19-SEP-2002; 2002WO-US029664.

XX PR 19-SEP-2001; 2001US-00956712.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Freier SM;

XX DR WPI; 2003-354583/33.

XX DR N-PSDB; ACC45152.

XX PT New antisense compounds, useful for modulating the expression of NAC or

XX PT for treating a disease or condition associated with the expression of

XX PT NAC, e.g. hyperproliferative disease or neurological disease.

XX PS Example 15; Page 121-128; 147pp; English.

XX CC The present invention describes a compound (I) 8-50 nucleobases in length

XX CC targeted to a nucleic acid molecule encoding NAC, where the compound

XX CC specifically hybridises with the nucleic acid molecule encoding NAC and

XX CC inhibits the expression of NAC. The compound specifically hybridises with

XX CC at least an 8-nucleobase portion of an active site on a nucleic acid

XX CC molecule encoding NAC. Also described: (1) a composition comprising (I)

XX CC and a pharmaceutical carrier or diluent; (2) inhibiting the expression of

XX CC NAC in cells or tissues comprising contacting the cells or tissues with

XX CC (I); and (3) treating an animal having a disease or condition associated

XX CC with NAC comprising administering (I) to the animal so that expression of

XX CC NAC is inhibited. (I) has cytostatic, neurotropic, neuroprotective and

XX CC antiinflammatory activities, and can be used in antisense therapy. The

XX CC antisense compounds (I) are useful for modulating the expression of NAC,

XX CC and for treating a disease or condition associated with expression of

XX CC NAC, e.g. hyperproliferative disease, neurological disease, or a disease

XX CC or disorder arising from aberrant apoptosis. The compounds are also

XX CC useful as research reagents and kits, or for diagnostics, therapeutics

CC and prophylaxis, e.g. to prevent or delay infection, inflammation or

CC tumour formation. NAC is also known as a death effector filament-forming

CC CED4-like apoptosis protein (DEFCAP). NAC is located on human chromosome

CC 17p13. The present sequence represents a human caspase recruitment domain

CC protein 7, which is used in an example from the invention

XX SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 6; Length 1429;

Best Local Similarity 100.0%; Pred. No. 2.2e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQMRKLFSLSQSWDR 60

DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQEQYERVLAEVTRPSQMRKLFSLSQSWDR 1394

QY 61 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 95

DB 1395 KCKDGLYQALKETHPHLMELWEGSKKGLPLSS 1429

RESULT 10

ABP96888

ID ABP96888 standard; protein; 1429 AA.

XX AC ABP96888;

XX DT 16-JUN-2003 (first entry)

XX DE Human NAC protein SEQ ID NO:3.

XX KW Human; cytostatic; neurotropic; neuroprotective; antiinflammatory;

XX KW antisense therapy; NAC; DEFCAP; hyperproliferative disease; apoptosis;

XX KW death effector filament-forming CED4-like apoptosis protein;

XX KW neurological disease; infection; inflammation; tumour formation;

XX KW chromosome 17p13.

XX OS Homo sapiens.

XX PN WO2003024988-A1.

XX PD 27-MAR-2003.

XX PF 19-SEP-2002; 2002WO-US029664.

XX PR 19-SEP-2001; 2001US-00956712.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Freier SM;

XX DR WPI; 2003-354583/33.

XX DR N-PSDB; ACC45143.

XX PT New antisense compounds, useful for modulating the expression of NAC or

XX PT for treating a disease or condition associated with the expression of

XX PT NAC, e.g. hyperproliferative disease or neurological disease.

XX PS Example 13; Page 81-88; 147pp; English.

XX CC The present invention describes a compound (I) 8-50 nucleobases in length

XX CC targeted to a nucleic acid molecule encoding NAC, where the compound

XX CC specifically hybridises with the nucleic acid molecule encoding NAC and

XX CC inhibits the expression of NAC. The compound specifically hybridises with

XX CC at least an 8-nucleobase portion of an active site on a nucleic acid

XX CC molecule encoding NAC. Also described: (1) a composition comprising (I)

XX CC and a pharmaceutical carrier or diluent; (2) inhibiting the expression of

XX CC NAC in cells or tissues comprising contacting the cells or tissues with

XX CC (I); and (3) treating an animal having a disease or condition associated

XX CC with NAC comprising administering (I) to the animal so that expression of

XX CC NAC is inhibited. (I) has cytostatic, neurotropic, neuroprotective and

XX CC antiinflammatory activities, and can be used in antisense therapy. The

XX CC antisense compounds (I) are useful for modulating the expression of NAC,

CC and for treating a disease or condition associated with expression of  
CC NAC, e.g. hyperproliferative disease, neurological disease, or a disease  
CC or disorder arising from aberrant apoptosis. The compounds are also  
CC useful as research reagents and kits, or for diagnostics, therapeutics  
CC and prophylaxis, e.g. to prevent or delay infection, inflammation or  
CC tumour formation. NAC is also known as a death effector filament-forming  
CC CD4-like apoptosis protein (DECAP). NAC is located on human chromosome  
CC 17p13. The present sequence represents human NAC, which is used in an  
CC example from the present invention

XX  
SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 6; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLQSQWDR 60  
DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLQSQWDR 1394

QY 61 KCKGGLYQALKETHPHLMELWEKSKGKGLPLSS 95  
DB 1395 KCKGGLYQALKETHPHLMELWEKSKGKGLPLSS 1429

RESULT 11  
ABG71633  
ID ABG71633 standard; protein; 1429 AA.  
XX  
AC ABG71633;  
XX  
DT 10-JAN-2003 (first entry)  
XX  
DE Human caspase recruitment domain-7 (CARD-7).  
XX  
KW Human; caspase activity; caspase recruitment domain-7; CARD-7; caspase-1;  
KW pseudo-interleukin-1 beta converting enzyme; IL-1beta; pseudoICE;  
KW ICEBERG; cell growth; cell death; inflammation; apoptosis;  
KW caspase activation; cancer; follicular lymphoma; leukaemia; melanoma;  
KW colon cancer; lung carcinoma; viral infection; autoimmune disease;  
KW systemic lupus erythematosus; reactive arthritis;  
KW human immunodeficiency virus infection; HIV infection; ALS;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW myocardial infarction; stroke; inflammatory disorder; Crohn's disease;  
KW insulin dependent diabetes mellitus; multiple sclerosis; psoriasis;  
KW graft rejection; allergic rhinitis; food allergy; conjunctivitis;  
KW glomerular nephritis; cytostatic; virucide; immunosuppressive;  
KW dermatological; nephrotropic; neuroprotective; cardiant.  
XX  
OS Homo sapiens.  
XX  
XX US2002128198-A1.  
XX  
XX 12-SEP-2002.  
XX  
XX 27-NOV-2001; 2001US-00996617.  
XX  
XX 28-JUN-1999; 99US-00340620.  
XX  
XX 27-OCT-1999; 99US-00428252.  
XX  
XX 15-AUG-2001; 2001US-00931071.  
XX  
XX (BERT)/ BERTIN J.  
XX  
XX Bertin J;  
XX  
XX WPI; 2003-028967/02.  
XX  
XX N-PSDB; ABS56030.  
XX  
XX Identifying modulator of CARD-7 and CARD-5 interaction, by contacting  
XX CARD-7 and CARD-5 in presence of test compound, measuring their binding,  
XX and identifying modulator, when binding of CARD-7 to CARD-5 is altered.  
XX  
XX Disclosure; Fig 1; 43pp; English.

XX The present invention relates to methods of identifying compounds that  
CC regulate caspase activity using caspase recruitment domain-7 (CARD-7) or  
CC caspase recruitment domain-8 (CARD-8). In particular, a method for  
CC identifying a compound that modulates the interaction between CARD-8 and  
CC caspase-1, pseudo-interleukin-1 (IL-1) beta converting enzyme (pseudoICE)  
CC or ICEBERG is disclosed. CARD-7 and CARD-8 molecules are useful as  
CC modulating agents in regulating a variety of cellular processes including  
CC cell growth, cell death, and inflammation. The methods of the invention  
CC are useful for identifying compounds that have the ability to  
CC increase/decrease apoptosis, or comprise the ability to induce caspase  
CC activation. The methods are useful for treating a disorder associated  
CC with inappropriate apoptosis or inappropriate inflammation. The methods  
CC are useful for treating disorders associated with an undesirably low rate  
CC of apoptosis such as cancer (preferably follicular lymphoma, chronic  
CC myelogenous leukaemia, melanoma, colon cancer, lung carcinoma, etc),  
CC (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis,  
CC and arthritis). The methods are also useful for treating disorders with  
CC undesirably high rates of apoptosis such as human immunodeficiency virus  
CC (HIV) infection, Alzheimer's disease, Parkinson's disease, amyotrophic  
CC lateral sclerosis (ALS), retinitis pigmentosa, spinal muscular atrophy,  
CC various forms of cerebellar degeneration, anaemia associated with chronic  
CC disease, aplastic anaemia, chronic neutropenia, myelodysplastic  
CC syndromes, myocardial infarction, stroke, and various inflammatory  
CC disorders (e.g. Crohn's disease, reactive arthritis, insulin dependent  
CC diabetes mellitus, multiple sclerosis, psoriasis, graft rejection,  
CC allergic rhinitis, food allergies, conjunctivitis, glomerular nephritis,  
CC etc). The present sequence represents human CARD-7

XX  
SQ Sequence 1429 AA;

Query Match 100.0%; Score 490; DB 6; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 2.2e-48;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLQSQWDR 60  
DB 1335 LHFVDQYREQLIARVTSVEVLDKLGQVLSQYQYERVLAEINTPSQMRKLFSLQSQWDR 1394

QY 61 KCKGGLYQALKETHPHLMELWEKSKGKGLPLSS 95  
DB 1395 KCKGGLYQALKETHPHLMELWEKSKGKGLPLSS 1429

RESULT 12  
AAV72671  
ID AAV72671 standard; protein; 1442 AA.  
XX  
XX AAV72671;  
XX  
XX 31-MAY-2001 (first entry)  
XX  
XX Human NB-ARC and CARD containing protein (NAC) delta isoform.  
XX  
XX Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;  
XX caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;  
XX cysteine aspartyl protease; apoptosis; cytokine production;  
XX cytokine receptor signalling; therapy; inflammatory disorder; sepsis;  
XX fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Region 1..956  
XX FT /note= "Corresponds to 1-956 residues of human NAC beta  
XX FT isoform (AAV72669)"  
XX FT 957..1442  
XX FT Region  
XX FT /note= "Corresponds to 988-1473 residues of human NAC  
XX FT beta isoform (AAV72669)"  
XX PN WO200116170-A2.  
XX

PD 08-MAR-2001.  
 XX  
 PF 01-SEP-2000; 2000WO-US024152.  
 XX  
 PR 01-SEP-1999; 99US-00388221.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC;  
 XX  
 DR WPI; 2001-183258/18.  
 DR N-PSDB; AAD02762.  
 XX  
 PT Novel nucleic acid encoding NB-ARC and caspase associated recruitment  
 PT domains, used to produce polypeptides for screening for modulators of  
 PT apoptosis.  
 XX  
 PS Claim 15; Page 154-158; 184pp; English.  
 XX  
 CC The present sequence is a human NB-ARC and CARD containing protein (NAC)  
 CC delta isoform. NAC delta isoform represents the NAC splice variant in  
 CC which one of the splice region is absent in the translated polypeptide.  
 CC NAC protein comprises a nucleotide binding (NB) domain (also referred as  
 CC NB-ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-  
 CC Barrel-like domain. The caspases, cysteine aspartyl proteases, are  
 CC principal effectors of apoptosis. CARD containing NAC proteins are used  
 CC for screening modulators that modulates apoptosis, cytokine production,  
 CC cytokine receptor signalling and other cellular processes. NAC can act as  
 CC an immunogen for the production of polyclonal and monoclonal antibodies.  
 CC It can also be used to diagnose and treat inflammatory disorders such as  
 CC sepsis, fibrosis and arthritis and cancer pathologies such as  
 CC adenocarcinomas and leukaemias  
 XX  
 SQ Sequence 1442 AA;  
 Query Match 100.0%; Score 490; DB 4; Length 1442;  
 Best Local Similarity 100.0%; Pred. No. 2-2e-48;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPSQMRKLFSLSQSWDR 60  
 DB 1348 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPSQMRKLFSLSQSWDR 1407  
 QY 61 KCKDGLYQALKETHPHLMELWEXGSKGLPLSS 95  
 DB 1408 KCKDGLYQALKETHPHLMELWEXGSKGLPLSS 1442  
 RESULT 13  
 AAE06758  
 ID AAE06758 standard; protein; 1473 AA.  
 AC AAE06758;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human G-protein coupled receptor-8 (GCREC-8) protein.  
 XX  
 KW Human; G-protein coupled receptor-8; GCREC-8; cytosolic; hepatotropic;  
 KW virulence; antiinflammatory; anticonvulsant; antiemetic; neuroprotective;  
 KW nontropic; cerebroprotective; hypotensive; tranquiliser; vulnery;  
 KW ophthalmological; cell proliferative disorder; actinic keratosis;  
 KW anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;  
 KW psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease;  
 KW Huntington's disease; Parkinson's disease; cardiovascular disorder;  
 KW epilepsy; hypertension; varicose vein; vasculitis; dyspepsia;  
 KW anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder;  
 KW Addison's disease; Crohn's disease; acquired immune deficiency syndrome;  
 KW AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity;  
 KW osteoporosis; transgenic animal; gene therapy.  
 OS Homo sapiens.  
 XX

PH Key Location/Qualifiers  
 FT Binding-site 334..341  
 FT /label= ATP/GTP-binding\_site  
 FT /note= "P-loop"  
 FT Domain 1216..1237  
 FT /label= Transmembrane\_domain  
 XX  
 PN WO200157085-A2.  
 XX  
 XX 09-AUG-2001.  
 PD  
 XX 01-FEB-2001; 2001WO-US003455.  
 PF  
 XX 02-FEB-2000; 2000US-0180093P.  
 PR 11-FEB-2000; 2000US-0182045P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Baughn MR, Au-Young J, Yue H;  
 PI WPI; 2001-488569/53.  
 DR N-PSDB; AAD12951.  
 DR  
 XX Novel isolated human G-protein coupled receptor useful for diagnosing,  
 PT preventing and treating cell proliferative, neurological, cardiovascular,  
 PT gastrointestinal, autoimmune/inflammatory and metabolic disorders.  
 XX  
 PS Claim 1; Page 114-117; 138pp; English.  
 XX  
 CC The present sequence is human G-protein coupled receptor-8 (GCREC-8)  
 CC protein. The present invention relates to GCREC protein and nucleic acids  
 CC encoding them. GCREC protein, its agonist or antagonist are useful for  
 CC treating diseases or conditions associated with decreased expression or  
 CC overexpression of functional GCREC in a patient, where the disorder is  
 CC selected from cell proliferative disorders such as actinic keratosis,  
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and  
 CC cancer, neurological disorders such as epilepsy, stroke, Alzheimer's  
 CC disease, Huntington's disease, Parkinson's disease, cardiovascular  
 CC disorders such as hypertension, vasculitis, varicose veins, gastro-  
 CC intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,  
 CC pancreatitis, autoimmune/inflammatory disorders such as acquired  
 CC immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease,  
 CC uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic  
 CC infections, trauma and metabolic disorders such as diabetes, obesity,  
 CC osteoporosis. GCREC proteins and their cDNAs are used to assess the  
 CC effects of exogenous compounds on the expression of GCREC sequences.  
 CC GCREC cDNA is useful to create knock in humanised animals (pigs) or  
 CC transgenic animals (mice or rats) to model human disease, for therapeutic  
 CC or diagnostic purposes, for somatic or germline gene therapy, to generate  
 CC hybridisation probes useful in mapping the naturally occurring genomic  
 CC sequence, and in molecular biological techniques  
 XX  
 SQ Sequence 1473 AA;  
 Query Match 100.0%; Score 490; DB 4; Length 1473;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-48;  
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPSQMRKLFSLSQSWDR 60  
 DB 1379 LHFVDQYREQLIARTVTSVEVLDKLGQVLSQEQYERVLAEINTPSQMRKLFSLSQSWDR 1438  
 QY 61 KCKDGLYQALKETHPHLMELWEXGSKGLPLSS 95  
 DB 1439 KCKDGLYQALKETHPHLMELWEXGSKGLPLSS 1473  
 RESULT 14  
 AAY72669  
 ID AAY72669 standard; protein; 1473 AA.  
 XX  
 AC AAY72669;  
 XX

DT XX 31-MAY-2001 (first entry)

DE XX Human NB-ARC and CARD containing protein (NAC) beta isoform.

KW Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;

KW caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;

KW cysteine aspartyl protease; apoptosis; cytokine production;

KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;

KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.

OS Homo sapiens.

PH Key Location/Qualifiers

FT 329..547

FT /label= NB domain

FT /note= "Nucleotide binding domain, also designated as

FT NB-ARC domain"

FT 329..341

FT /label= Walker\_A

FT /note= "Also designated as P-loop"

FT 406..414

FT /label= Walker\_B

FT 809..833

FT /label= Leucine\_rich\_repeat\_region

FT 838..862

FT /label= Leucine\_rich\_repeat\_region

FT 865..890

FT /label= Leucine\_rich\_repeat\_region

FT 895..919

FT /label= Leucine\_rich\_repeat\_region

FT 923..947

FT /label= Leucine\_rich\_repeat\_region

FT 957..987

FT /note= "This 31 amino acid segment is not found in NAC

FT gamma isoform (AAY72670) and NAC delta isoform (AAY72671)

FT due to alternative mRNA splicing"

FT 1079..1364

FT /note= "TIM-Barrel-like domain"

FT 1128..1473

FT /label= CARD-L

FT /note= "Caspase-associated recruitment domain"

FT 1128..1261

FT /label= CARD-S

FT /note= "Caspase-associated recruitment domain"

FT 1261..1306

FT /note= "This 45 amino acid segment is not found in NAC

FT gamma isoform (AAY72670) due to alternative mRNA

FT splicing"

FT 1306..1473

FT /label= CARD-S

FT /note= "Caspase-associated recruitment domain"

FT 1373..1473

FT /label= CARD

FT /note= "Caspase-associated recruitment domain"

XX WO2000116170-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-US024152.

XX 01-SEP-1999; 99US-00388221.

XX (BURN-) BURNHAM INST.

XX Read JC;

XX WPI; 2001-183258/18.

XX N-PSDB; AAD02760.

XX Novel nucleic acid encoding NB-ARC and caspase associated recruitment

XX domains, used to produce polypeptides for screening for modulators of

XX apoptosis.

XX Claim 15; Page 133-137; 184pp; English.

XX The present sequence is a human NB-ARC and CARD containing protein (NAC)

CC beta isoform. NAC beta isoform represents the NAC splice variant in which

CC both the splice regions are present in the translated polypeptide. NAC

CC protein comprises a nucleotide binding (NB) domain (also referred as NB-

CC ARC domain), a caspase-associated recruitment domain (CARD) and a TIM-

CC Barrel-like domain. The caspases, cysteine aspartyl proteases, are

CC principal effectors of apoptosis. CARD containing NAC proteins are used

CC for screening modulators that modulates apoptosis, cytokine production,

CC cytokine receptor signalling and other cellular processes. NAC can act as

CC an immunogen for the production of polyclonal and monoclonal antibodies.

CC It can also be used to diagnose and treat inflammatory disorders such as

CC sepsis, fibrosis and arthritis and cancer pathologies such as

CC adenocarcinomas and leukaemias. Note: This sequence is stated as being

CC the same as that shown as SEQ ID NO:2 (AAY72711) in figure 1A of the

CC specification. However the sequences differ at several positions

XX CC

SQ Sequence 1473 AA;

Query Match 100.0%; Score 490; DB 4; Length 1473;

Best Local Similarity 100.0%; Pred. No. 2.3e-48;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHFVDQYREQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTRPSQMKLFSLQSQWDR 60

DB 1379 LHFVDQYREQLIARTVTSVEVLDKLHGQVLSQEQYERVLAEINTRPSQMKLFSLQSQWDR 1438

QY 61 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 95

DB 1439 KCKDGLYQALKETHPHLMELWEKSKKGLPLSS 1473

RESULT 15

AAY72711

ID AAY72711 standard; protein; 1473 AA.

XX AC AAY72711;

XX 31-MAY-2001 (first entry)

XX Human NAC beta isoform, alternative version.

DE Human; NB domain; nucleotide binding domain; NB-ARC and CARD; NAC;

XX caspase-associated recruitment domain; CARD; TIM-Barrel-like domain;

KW cysteine aspartyl protease; apoptosis; cytokine production;

KW cytokine receptor signalling; therapy; inflammatory disorder; sepsis;

KW fibrosis; arthritis; cancer; adenocarcinoma; leukaemia.

XX Homo sapiens.

OS Key Location/Qualifiers

PH Key 329..547

FT Domain /label= NB domain

FT /note= "Nucleotide binding domain, also designated as

FT NB-ARC domain"

FT 329..341

FT /label= Walker\_A

FT /note= "Also designated as P-loop"

FT 406..414

FT /label= Walker\_B

FT 809..833

FT /label= Leucine\_rich\_repeat\_region

FT 838..862

FT /label= Leucine\_rich\_repeat\_region

FT 865..890

FT /label= Leucine\_rich\_repeat\_region

FT 895..919

FT /label= Leucine\_rich\_repeat\_region

FT 923..947

FT /label= Leucine\_rich\_repeat\_region

FT 957..987



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:11 ; Search time 41.0602 Seconds  
(without alignments)  
488.572 Million cell updates/sec

Title: US-09-996-617-8\_COPY\_111\_181

Perfect score: 378  
Sequence: 1 GLHFIDQHRALIAIVTNVE.....LFSFTPAWNTCKDLLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Genesecp1980s:\*  
2: Genesecp1980s:\*  
3: Genesecp2000s:\*  
4: Genesecp2001s:\*  
5: Genesecp2002s:\*  
6: Genesecp2003as:\*  
7: Genesecp2003bs:\*  
8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	176	AAE00594	Aae00594 Alternati
2	378	100.0	195	AAy48553	Aay48553 Human bre
3	378	100.0	195	AAU68525	Aau68525 Human nov
4	378	100.0	195	AAb20085	Aab20085 Human CAR
5	378	100.0	195	AAE00588	Aae00588 Human tar
6	378	100.0	195	AAU99353	Aau99353 Human cas
7	378	100.0	195	AAO17854	Aao17854 Pryn dom
8	378	100.0	195	ABG71635	Abg71635 Human cas
9	378	100.0	205	AAg74647	Aag74647 Human col
10	372	98.4	84	AAE00591	Aae00591 Human tar
11	275	72.8	171	AAE00593	Aae00593 Rat targe
12	264	69.8	193	AAE20086	Aae20086 Mouse CAR
13	264	69.8	193	AAE00592	Aae00592 Mouse tar
14	264	69.8	193	AAU99352	Aau99352 Mouse cas
15	216	57.1	442	AAb24513	Aab24513 Human sec
16	216	57.1	1397	AAy72670	Aay72670 Human NB-
17	216	57.1	1429	AAb62571	Aab62571 Human CAR
18	216	57.1	1429	ABg78455	Abg78455 Human cas
19	216	57.1	1429	ABg78472	Abg78472 Leucine-r
20	216	57.1	1429	ABB77916	Abb77916 Human leu
21	216	57.1	1429	ABg97969	Abg97969 Human leu
22	216	57.1	1429	AAO17855	Aao17855 Pryn dom
23	216	57.1	1429	ABG71631	Abg71631 Human cas
24	216	57.1	1429	ABP96889	Abp96889 Human cas
25	216	57.1	1429	ABP96888	Abp96888 Human NAC

26	216	57.1	1429	6	ABG71633	Abg71633 Human cas
27	216	57.1	1442	4	AAy72671	Aay72671 Human NB-
28	216	57.1	1473	4	AAE06758	Aae06758 Human G-p
29	216	57.1	1473	4	AAy72669	Aay72669 Human NB-
30	216	57.1	1473	4	AAy72711	Aay72711 Human NAC
31	214	56.6	158	4	AAg74648	Aag74648 Human col
32	214	56.6	190	3	AAb43675	Aab43675 Human can
33	141	37.3	65	3	AAb24519	Aab24519 Human sec
34	75	19.8	59	3	AAb24520	Aab24520 Human sec
35	69.5	18.4	93	5	ABJ04755	Abj04755 ARC prote
36	69.5	18.4	208	6	ABR58613	Abr58613 Human can
37	69.5	18.4	219	7	ADD48044	Add48044 Human pro
38	68.5	18.1	230	4	AAU21812	Aau21812 Novel
39	68.5	18.1	230	7	ADC46453	Adc46453 Human neo
40	68.5	18.1	431	4	AAb62572	Aab62572 Human CAR
41	68.5	18.1	431	4	AAy72672	Aay72672 Human CAR
42	68.5	18.1	431	6	ABU03496	Abu03496 Angiogene
43	68.5	18.1	431	6	ABG71632	Abg71632 Human cas
44	68.5	18.1	431	6	ABB82736	Abb82736 Human TUC
45	68.5	18.1	431	6	ABG71634	Abg71634 Human cas

ALIGNMENTS

RESULT 1  
AAE00594  
ID AAE00594 standard; protein; 176 AA.

XX AC AAE00594;

XX DT 02-JUL-2001 (first entry)

XX DE Alternatively spliced form of human TMS1 protein (lacking exon2).  
XX Human; target of methylation-induced silencing-1; TMS1; cytostatic;  
XX antiproliferative; apoptosis inducer; gene therapy; CpG island;  
XX caspase-recruiting domain; CARD; cancer; breast.

XX OS Homo sapiens.

XX PN WO200129235-A2.

XX PD 26-APR-2001.

XX PF 18-OCT-2000; 2000WO-US028747.

XX PR 18-OCT-1999; 99US-0159975P.

XX (UYEM-) UNIV EMORY.

XX PI Vertino PM;

XX DR WPI; 2001-290922/30.

XX N-PSDB; AAD03906.

XX Novel gene TMS1, transcriptionally silenced due to increased methylation  
XX useful for identifying subject at risk of developing tumor characterized  
XX by abnormal methylation, for treating cancer by inducing apoptosis.

XX Claim 85; Page 123; 124pp; English.

XX The invention relates to identification of target of methylation-induced  
XX silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to  
XX abnormal methylation of a CpG island in its 5' regulatory region. TMS1  
XX consists of a carboxy terminal caspase-recruiting domain (CARD) and plays  
XX a role in induction of apoptosis. TMS1 gene and protein are useful as  
XX tools for diagnosing and treating a subject at risk of developing cancer  
XX (e.g. breast cancer) characterised by abnormal CpG methylation or  
XX abnormally low levels of TMS1 expression products. Unique fragments of  
XX TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1  
XX molecule is also useful for treating abnormal cell proliferation by  
XX increasing TMS1 polypeptide level to an above normal level. The Cpg

CC island region of TMS1 or its fragments are used to study the methylation  
CC patterns apart from any coding region contained in it. The present  
CC sequence is alternatively spliced form of human target of methylation-  
CC induced silencing-1 (TMS1) protein lacking exon2  
XX  
SQ Sequence 176 AA;  
Query Match 100.0%; Score 378; DB 4; Length 176;  
Best Local Similarity 100.0%; Pred. No. 3.2e-40;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLHFIDQHRRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60  
DB 92 GLHFIDQHRRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 151  
QY 61 WTCKDLLLQAL 71  
DB 152 WTCKDLLLQAL 162  
RESULT 2  
ID AAY48553 standard; protein; 195 AA.  
AC AAY48553;  
XX  
XX 08-DEC-1999 (first entry)  
DE Human breast tumour-associated protein 14.  
XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;  
KW treatment; tumour; cytostatic; medicament.  
XX  
XX Homo sapiens.  
XX  
XX DE19813839-A1.  
XX  
XX 23-SEP-1999.  
XX  
XX 20-MAR-1998; 98DE-01013839.  
XX  
XX 20-MAR-1998; 98DE-01013839.  
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.  
XX  
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;  
PI WPI; 1999-528981/45.  
DR N-PSDB; AAZ33631.  
XX  
XX Human nucleic acid sequences and protein products from tumor breast  
PT tissue, useful for breast cancer therapy.  
XX  
XX Claim 22; 149; 188pp; German.  
XX  
XX This invention describes novel human nucleic acid sequences from tumor  
CC breast tissue which have cytostatic activity. The nucleic acid sequences  
CC can be used to produce and isolate full-length gene sequences. They can  
CC be used to express proteins, which can be used as tools to find an  
CC activity against breast cancer. The sequences can be used in sense or  
CC antisense form. They are especially useful for medicaments for gene  
CC therapy to treat breast cancer. AAY48540-Y48617 represent protein  
CC fragments encoded by the expressed sequence tags described in the method  
CC of the invention  
XX  
SQ Sequence 195 AA;  
Query Match 100.0%; Score 378; DB 2; Length 195;  
Best Local Similarity 100.0%; Pred. No. 3.7e-40;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GLHFIDQHRRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

DB 111 GLHFIDQHRRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170  
QY 61 WTCKDLLLQAL 71  
DB 171 WTCKDLLLQAL 181  
RESULT 3  
ID AAY68525 standard; protein; 195 AA.  
XX  
XX AAY68525;  
XX  
XX 16-JAN-2002 (first entry)  
XX Human novel cytokine encoded by cDNA 790CIP2B\_1 #1.  
XX Human; cytokine; cell proliferation; cell differentiation;  
KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;  
KW nervous system disease; neuropathy; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; spinal cord disorder;  
KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;  
KW platelet disorder; thrombocytopaenia; stem cell disorder;  
KW aplastic anaemia; tissue regeneration; wound healing; ulcer;  
KW osteoporosis; osteoarthritis; bone degenerative disorder;  
KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;  
KW severe combined immunodeficiency; infection; autoimmune disorder;  
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;  
KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;  
KW inflammatory bowel disease; food supplement; immunogen.  
XX  
XX Homo sapiens.  
XX  
XX WO200175093-A1.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US010484.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX 22-SEP-2000; 2000US-00668680.  
XX 23-OCT-2000; 2000US-00655618.  
XX 30-NOV-2000; 2000US-00728711.  
XX 14-MAR-2001; 2001US-00808701.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
PI Xu C, Yang Y, Zhao QA, Chen R, Wang D, Goodrich RW, Liu C;  
PI Drmanac RT;  
XX  
XX WPI; 2001-626432/72.  
DR N-PSDB; AAG59817.  
XX  
XX New polypeptides and nucleic acids, useful for diagnosis, treatment of  
PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone  
PT degenerative disorders, cancer and promoting wound healing.  
XX  
XX Claim 20; Page 242-243; 336pp; English.  
XX  
XX The invention relates to isolated human polypeptides (which may be  
CC cytokines) and the polynucleotides encoding them. The protein is useful  
CC for identifying a compound which binds to it (e.g. modulators, agonists  
CC and antagonists). The polynucleotides are useful as an array for mismatch  
CC detection. The proteins and nucleic acids are useful as nutritional  
CC sources or supplements. The protein exhibits activity relating  
CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,  
CC stem cell growth factor activity, immune stimulating or immune  
CC suppressing and activin or inhibin related activities. The proteins (and  
CC antibodies raised against them) and nucleic acids are therefore useful in  
CC the diagnosis and treatment of diseases and disorders such as cancer,  
CC central and peripheral nervous system diseases and neuropathies,



CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular  
 CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,  
 CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for  
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
 CC growth, and in tissue repair, healing of burns, incisions, ulcers, for  
 CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or  
 CC periodontal disease, lung or liver fibrosis, reperfusion injury in  
 CC various tissues, various immune deficiencies and disorders including  
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,  
 CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,  
 CC diabetes mellitus, myasthenia gravis), allergic reactions and conditions,  
 CC such as asthma or other respiratory problems, coagulation disorders,  
 CC haemophilial, septic shock, sepsis, arthritis, nephritis and inflammatory  
 CC bowel disease, viral infection and are useful in altering bodily  
 CC characteristics. The present sequence represents a novel protein of the  
 CC invention  
 XX  
 SQ Sequence 195 AA;

Query Match 100.0%; Score 378; DB 4; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-40;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRALIARVTVNVEWLLDALYGVLTDSQYQAVRAEPTNPSKMKLFSTPAWN 60  
 DB 111 GLHFIDQHRALIARVTVNVEWLLDALYGVLTDSQYQAVRAEPTNPSKMKLFSTPAWN 170  
 QY 61 WTCKDLLLQAL 71  
 DB 171 WTCKDLLLQAL 181

RESULT 4  
 AAB20085  
 ID AAB20085 standard; protein; 195 AA.

XX  
 AC AAB20085;  
 DT 23-APR-2001 (first entry)  
 DE Human CARD-5 protein.  
 KW CARD-5; caspase recruitment domain; human; cancer; infection;  
 KW autoimmune disease; neurological disease; haematological disease;  
 KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
 KW anti-inflammatory; apoptosis; diagnosis; gene therapy.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Domain 111..181  
 FT /note= "CARD"  
 XX  
 XX WO200100826-A2.  
 XX  
 XX 04-JAN-2001.  
 XX  
 XX 28-JUN-2000; 2000WO-US017691.  
 XX  
 XX 28-JUN-1999; 99US-00340620.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Bertin J;  
 XX  
 XX WPI; 2001-061973/07.  
 XX N-PSDB; AAF30007.  
 XX  
 XX Isolated intracellular proteins predicted to be involved in regulating  
 XX caspase activation are used for diagnosis and treatment of e.g. cancer,  
 XX viral infections, autoimmune diseases, neurological diseases and  
 XX hematological disorders.

XX Claim 9; Fig 21; 208pp; English.

XX The present sequence is that of human caspase recruitment domain 5 (CARD-5), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF30007). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using gene therapy methods. Such disorders include cancer, viral infection, CC autoimmune disorders, neurological diseases, haematological disorders, CC inflammatory disorders and immune disorders, CARD-3, -4, -5 and -6 CC proteins can be used to regulate cell proliferation, cell survival and CC cell growth. They can also be used to screen drugs or compounds that CC modulate their activity or expression and to treat disorders associated CC with insufficient or excessive production of CARD-3, -4, -5 or -6 CC protein, or production of an aberrant protein  
 XX  
 SQ Sequence 195 AA;

Query Match 100.0%; Score 378; DB 4; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-40;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRALIARVTVNVEWLLDALYGVLTDSQYQAVRAEPTNPSKMKLFSTPAWN 60  
 DB 111 GLHFIDQHRALIARVTVNVEWLLDALYGVLTDSQYQAVRAEPTNPSKMKLFSTPAWN 170  
 QY 61 WTCKDLLLQAL 71  
 DB 171 WTCKDLLLQAL 181

RESULT 5  
 AAE00588  
 ID AAE00588 standard; protein; 195 AA.

XX  
 AC AAE00588;  
 XX  
 DT 02-JUL-2001 (first entry)  
 DE Human target of methylation-induced silencing-1 (TMS1) protein.  
 XX  
 KW Human; target of methylation-induced silencing-1; TMS1; cytostatic;  
 KW antiproliferative; apoptosis inducer; gene therapy; CpG island;  
 KW caspase-recruiting domain; CARD; cancer; breast.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200129235-A2.  
 XX  
 XX 26-APR-2001.  
 XX  
 XX 18-OCT-2000; 2000WO-US028747.  
 XX  
 XX 18-OCT-1999; 99US-0159975P.  
 XX  
 XX (UYEM-) UNIV EMORY.  
 XX  
 XX Vertino PW;  
 XX  
 XX WPI; 2001-290922/30.  
 XX N-PSDB; AAD03889; AAD03890.  
 XX  
 XX Novel gene TMS1, transcriptionally silenced due to increased methylation  
 XX useful for identifying subject at risk of developing tumor characterized  
 XX by abnormal methylation, for treating cancer by inducing apoptosis.  
 XX  
 XX Claim 85; Page 114; 124pp; English.





XX AC AAG74647;  
 XX DT 03-SEP-2001 (first entry)  
 XX DE Human colon cancer antigen protein SEQ ID NO:5411.  
 XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 XX KW colorectal carcinoma.  
 XX OS Homo sapiens.  
 XX PN WO200122920-A2.  
 XX PD 05-APR-2001.  
 XX PF 28-SEP-2000; 2000WO-US026524.  
 XX PR 29-SEP-1999; 99US-0157137P.  
 XX PR 03-NOV-1999; 99US-0163280P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 XX WPI: 2001-235357/24.  
 XX N-PSDB; AAH34052.  
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers.  
 XX Claim 11; Page 7035-7036; 9803pp; English.  
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
 CC proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene therapy  
 CC and vaccine production. N and P may be used in the prevention, diagnosis  
 CC and treatment of diseases associated with inappropriate P expression. For  
 CC example, N and P may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of P by expressing inactive proteins or to  
 CC supplement the patients own production of P. Additionally, N may be used  
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the proteins. N and P  
 CC can be used in the prevention, diagnosis and treatment of colorectal  
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
 CC sequences used in the exemplification of the present invention. N.B.  
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
 CC to 1052, 7921 and 7922  
 XX Sequence 205 AA;  
 SQ  
 Query Match 100.0%; Score 378; DB 4; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-40;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLHFDQHRAALIAIARTVNVVLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60  
 DB 121 GLHFDQHRAALIAIARTVNVVLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 180  
 QY 61 WTKDILLQAL 71  
 DB 181 WTKDILLQAL 191  
 RESULT 10  
 ID AA000591  
 AA000591 standard; protein; 84 AA.  
 XX AC AA000591;  
 XX DE Rat target of methylation-induced silencing-1 (TMS1) partial protein.  
 XX KW Rat; target of methylation-induced silencing-1; TMS1; cytostatic;

DT 02-JUL-2001 (first entry)  
 XX DE Human target of methylation-induced silencing-1 (TMS1) exon3 protein.  
 XX KW Human; target of methylation-induced silencing-1; TMS1; cytostatic;  
 KW antiproliferative; apoptosis inducer; gene therapy; CpG island;  
 KW caspase-recruiting domain; CARD; cancer; breast.  
 XX OS Homo sapiens.  
 XX PN WO200129235-A2.  
 XX PD 26-APR-2001.  
 XX PF 18-OCT-2000; 2000WO-US028747.  
 XX PR 18-OCT-1999; 99US-0159975P.  
 XX PA (UYEM-) UNIV EMORY.  
 XX PI Vertino PM;  
 XX WPI: 2001-290922/30.  
 XX N-PSDB; AAD03894.  
 XX Novel gene TMS1, transcriptionally silenced due to increased methylation  
 PT useful for identifying subject at risk of developing tumor characterized  
 PT by abnormal methylation, for treating cancer by inducing apoptosis.  
 XX Claim 25; Page 117; 124pp; English.  
 XX The invention relates to identification of target of methylation-induced  
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to  
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1  
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays  
 CC a role in induction of apoptosis. TMS1 gene and protein are useful as  
 CC tools for diagnosing and treating a subject at risk of developing cancer  
 CC (e.g. breast cancer) characterised by abnormal CpG methylation or  
 CC abnormally low levels of TMS1 expression products. Unique fragments of  
 CC TMS1 gene are also useful for treating abnormal cell proliferation by  
 CC increasing TMS1 polypeptide level to an above normal level. The CpG  
 CC island region of TMS1 or its fragments are used to study the methylation  
 CC patterns apart from any coding region contained in it. The present  
 CC sequence is human target of methylation-induced silencing-1 (TMS1) exon3  
 XX protein  
 XX Sequence 84 AA;  
 SQ  
 Query Match 98.4%; Score 372; DB 4; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-40;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LHFIDQHRAALIAIARTVNVVLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 61  
 DB 1 LHFIDQHRAALIAIARTVNVVLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60  
 QY 62 TCKDILLQAL 71  
 DB 61 TCKDILLQAL 70  
 RESULT 11  
 ID AA000593  
 AA000593 standard; protein; 171 AA.  
 XX AC AA000593;  
 XX DE Rat target of methylation-induced silencing-1 (TMS1) partial protein.  
 XX KW Rat; target of methylation-induced silencing-1; TMS1; cytostatic;

KW antiproliferative; apoptosis inducer; gene therapy; CpG island;  
 KW caspase-recruiting domain; CARD; cancer; breast.  
 XX  
 OS Rattus norvegicus.

XX  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 36  
 FT /note= "Encoded by AGY"  
 XX  
 XX

XX WO200129235-A2.

XX 26-APR-2001.

XX 18-OCT-2000; 2000WO-US028747.

XX 18-OCT-1999; 99US-0159975P.

XX (UYEM-) UNIV EMORY.

XX Vertino PM;

XX WPI; 2001-290922/30.

XX N-PSDB; AAD03905.

XX Novel gene TMS1, transcriptionally silenced due to increased methylation  
 PT useful for identifying subject at risk of developing tumor characterized  
 PT by abnormal methylation, for treating cancer by inducing apoptosis.  
 XX

PS Claim 85; Page 121; 124pp; English.

XX The invention relates to identification of target of methylation-induced  
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to  
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1  
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays  
 CC a role in induction of apoptosis. TMS1 gene and protein are useful as  
 CC tools for diagnosing and treating a subject at risk of developing cancer  
 CC (e.g. breast cancer) characterized by abnormal CpG methylation or  
 CC abnormally low levels of TMS1 expression products. Unique fragments of  
 CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1  
 CC molecule is also useful for treating abnormal cell proliferation by  
 CC increasing TMS1 polypeptide level to an above normal level. The CpG  
 CC island region of TMS1 or its fragments are used to study the methylation  
 CC patterns apart from any coding region contained in it. The present  
 CC sequence is rat target of methylation-induced silencing-1 (TMS1) partial  
 CC protein  
 XX

SQ Sequence 171 AA;

Query Match 72.8%; Score 275; DB 4; Length 171;  
 Best Local Similarity 76.8%; Pred. No. 5.4e-27;  
 Matches 53; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAVTNVWELLDALYGVLTDEQYQAVRAEPTNPSKVKLFPSFTPAWNT 62  
 DB 89 HFVDQHRQALIAVTNVWELLDALYGVLTDEQYQAVRAEPTNPSKVKLFPSFTPAWNT 148

QY 63 CKDILLQAL 71  
 DB 149 CKNLFLEAL 157

RESULT 12

AAB20086

ID AAB20086 standard; protein; 193 AA.

XX AAB20086;

XX 23-APR-2001 (first entry)

XX Mouse CARD-5 protein.

XX CARD-5; caspase recruitment domain; mouse; cancer; infection;  
 KW autoimmune disease; neurological disease; haematological disease;

KW immune disease; inflammation; antitumour; antiseptic; immunomodulator;  
 KW antiinflammatory; apoptosis; diagnosis; gene therapy.  
 XX  
 OS Mus sp.

XX  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 110..179  
 FT /note= "CARD"  
 XX  
 XX

XX WO200100826-A2.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US017691.

XX 28-JUN-1999; 99US-00340620.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin J;

XX WPI; 2001-061973/07.

XX N-PSDB; AAF30008.

XX Isolated intracellular proteins predicted to be involved in regulating  
 PT caspase activation are used for diagnosis and treatment of e.g. cancer,  
 PT viral infections, autoimmune diseases, neurological diseases and  
 PT hematological disorders.  
 XX

PS Claim 9; Fig 19; 208pp; English.

XX The present sequence is that of mouse caspase recruitment domain 5 (CARD-  
 CC 5), an intracellular protein predicted to be involved in regulating  
 CC caspase activation. The sequence is predicted from an isolated cDNA clone  
 CC (see AAF30008). It shows 71.8% amino acid identity to human CARD-5 (see  
 CC AAB20085). Methods of diagnosing and treating patients suffering from a  
 CC disorder associated with an abnormal level or rate of apoptotic cell  
 CC death, abnormal activity of the Fas/APO-1 receptor complex, abnormal  
 CC activity of the tumour necrosis factor receptor complex or abnormal  
 CC activity of a caspase involve administering a compound that modulates the  
 CC expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 e.g. using  
 CC gene therapy methods. Such disorders include cancer, viral infection,  
 CC autoimmune disorders, neurological diseases, haematological disorders,  
 CC inflammatory disorders and immune disorders. CARD-3, -4, -5 and -6  
 CC proteins can be used to regulate cell proliferation, cell survival and  
 CC cell growth. They can also be used to screen drugs or compounds that  
 CC modulate their activity or expression and to treat disorders associated  
 CC with insufficient or excessive production of CARD-3, -4, -5 or -6  
 CC protein, or production of an aberrant protein  
 XX

SQ Sequence 193 AA;

Query Match 69.8%; Score 264; DB 4; Length 193;  
 Best Local Similarity 73.9%; Pred. No. 1.6e-25;  
 Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAVTNVWELLDALYGVLTDEQYQAVRAEPTNPSKVKLFPSFTPAWNT 62  
 DB 111 HFVDQHRQALIAVTNVWELLDALYGVLTDEQYQAVRAEPTNPSKVKLFPSFTPAWNT 170

QY 63 CKDILLQAL 71

DB 171 CKDSLQAL 179

RESULT 13

AAE00592

ID AAE00592 standard; protein; 193 AA.

XX AAE00592;

XX 02-JUL-2001 (first entry)

XX

DE Mouse target of methylation-induced silencing-1 (TMS1) protein.  
XX Mouse; target of methylation-induced silencing-1, TMS1; cytostatic;  
KW antiproliferative; apoptosis inducer; gene therapy; CpG island;  
KW caspase-recruiting domain; CARD; cancer; breast.  
XX  
XX OS Mus musculus.  
XX WO2001:29235-A2.  
XX PD 26-APR-2001.  
XX PF 18-OCT-2000; 2000WO-US028747.  
XX PR 18-OCT-1999; 99US-0159975P.  
XX PA (UYEM-) UNIV EMORY.  
XX PT Vertino PM;  
XX PI WPI; 2001-290922/30.  
XX DR N-PSDB; AAD03904.  
XX CC Novel gene TMS1, transcriptionally silenced due to increased methylation  
PT useful for identifying subject at risk of developing tumor characterized  
PT by abnormal methylation, for treating cancer by inducing apoptosis.  
XX  
XX Claim 85; Page 120; 124pp; English.  
XX  
XX The invention relates to identification of target of methylation-induced  
CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to  
CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1  
CC consists of a carboxy terminal caspase-recruiting domain (CARD) and plays  
CC a role in induction of apoptosis. TMS1 gene and protein are useful as  
CC tools for diagnosing and treating a subject at risk of developing cancer  
CC (e.g. breast cancer) characterized by abnormal CpG methylation or  
CC abnormally low levels of TMS1 expression products. Unique fragments of  
CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy. TMS1  
CC molecule is also useful for treating abnormal cell proliferation by  
CC increasing TMS1 polypeptide level to an above normal level. The CpG  
CC island region of TMS1 or its fragments are used to study the methylation  
CC patterns apart from any coding region contained in it. The present  
CC sequence is mouse target of methylation-induced silencing-1 (TMS1)  
CC protein.  
XX  
XX Sequence 193 AA;  
Query Match 69.8%; Score 264; DB 4; Length 193;  
Best Local Similarity 73.9%; Pred. No. 1.6e-25;  
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;  
QY 3 HFICQRAALFARVTVNEMLDALYGVLDLDEQYQAVRABPTNPSKMRKLFSTPAWNT 62  
DB 111 HFVQHQALFARVTEVDGVLDLHGSVLTEGQYQAVRABPTTSDQRKLFSTFVPSNLT 170  
QY 63 CKDLLLQAL 71  
DB 171 CKDSLQAL 179  
RESULT 14  
AAU99352  
ID AAU99352 standard; protein; 193 AA.  
AC AAU99352;  
XX 07-OCT-2002 (first entry)  
XX Mouse caspase recruitment domain-5 (CARD-5) protein.  
XX Mouse; caspase recruitment domain-5; CARD-5; antiinflammatory;  
KW immunosuppressive; caspase; cysteinyl aspartate-specific proteinase;  
KW apoptosis; nuclear factor-kappa B; NF-kappaB; transcription factor;  
KW

KW cell proliferation; gene therapy; immune disorder;  
KW chronic inflammatory disease; Hashimoto's thyroiditis; graft rejection;  
KW sarcoidosis; atopy; asthma; allergy; glomerular nephritis;  
KW human immunodeficiency virus; HIV; bacterial infection; tuberculosis;  
KW lepromatous leprosy; autoimmune disorder; systemic lupus erythematosus;  
KW arthritis; cell depletion; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; spinal muscular atrophy; haematologic disease;  
KW myelodysplastic syndrome; aplastic anaemia; myocardial infarction;  
KW stroke.  
XX  
XX Mus sp.  
XX OS  
XX FH Key Location/Qualifiers  
FT Domain 110..193  
FT /label= CARD\_domain  
XX WO200244354-A2.  
XX PD 06-JUN-2002.  
XX PF 29-NOV-2001; 2001WO-US044894.  
XX PR 01-DEC-2000; 2000US-00728721.  
XX PR 24-APR-2001; 2001US-00841879.  
XX PA (MILL-) MILLENIUM PHARM INC.  
XX PI Bertin J;  
XX DR WPI; 2002-557538/59.  
XX DR N-PSDB; ABK87964.  
XX PT Novel isolated murine or human caspase recruitment domain (CARD)-5  
PT polypeptide, useful for treating immune disorders such as Hashimoto's  
PT thyroiditis, graft rejection, allergy, glomerular nephritis,  
PT tuberculosis.  
XX  
XX Claim 22; Fig 1; 100pp; English.  
XX The invention discloses the isolated polypeptides, and encoding nucleic  
CC acids, of murine and human caspase recruitment domain (CARD)-5. Caspases  
CC (cysteine aspartate-specific proteinases) are central to the apoptotic  
CC program and responsible for the degradation of cellular proteins that  
CC lead to the morphological changes seen in cells undergoing apoptosis.  
CC Caspases interact with other caspases via their CARDS and different  
CC subtypes of CARDS may confer binding specificity. CARD-5 is an  
CC intracellular protein that is predicted to be involved in regulating  
CC caspase activation. CARD-5 activates the nuclear factor-kappa B (NF-  
CC kappaB) transcription factor pathway and binds the CARDS of caspase-1,  
CC CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5 activity and NF  
CC -kappaB activation, regulate cell growth and cell death and be used in  
CC gene therapy. The CARD-5 polypeptides are useful for identifying  
CC compounds which bind to them and modulate their activity and for  
CC detecting the presence of CARD-5 in a sample. CARD-5 polypeptides,  
CC nucleic acids, antibodies and modulators of CARD-5 expression or activity  
CC can be used to treat immune disorders such as chronic inflammatory  
CC diseases and disorders, Hashimoto's thyroiditis, graft rejection,  
CC sarcoidosis, atopic conditions (such as asthma and allergy), glomerular  
CC nephritis, human immunodeficiency virus (HIV) and bacterial infections  
CC (including tuberculosis and lepromatous leprosy) and in screening and  
CC detection assays. Modulators of CARD-5 activity or expression are also  
CC useful for treating autoimmune disorders, such as systemic lupus  
CC erythematosus and arthritis, cell depletion, neurological disorders, such  
CC as Alzheimer's disease, Parkinson's disease and spinal muscular atrophy,  
CC haematologic diseases, such as myelodysplastic syndrome and aplastic  
CC anaemia, myocardial infarction and stroke. The sequence presented is the  
CC mouse caspase recruitment domain-5 (CARD-5) protein  
XX  
XX Sequence 193 AA;  
Query Match 69.8%; Score 264; DB 5; Length 193;  
Best Local Similarity 73.9%; Pred. No. 1.6e-25;  
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQHRRAALIAVTNNVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSTPAWNWT 62  
Db 111 HFVDQHRRAALIAVTNNVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSTPAWNWT 61  
QY 63 CKDLLLQAL 71  
Db 171 CKDGLYQAL 179

RESULT 15  
AAB24513  
ID AAB24513 standard; protein; 442 AA.  
XX AAB24513;  
XX DT 20-NOV-2000 (first entry)  
XX DE Human secreted protein sequence encoded by gene 12 SEQ ID NO:139.  
XX KW Human; secreted protein; cytostatic; antianaemic; antidiabetic;  
KW antiinflammatory; ophthalmological; antirheumatic; antiarthritic;  
KW antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic;  
KW neuroprotective; antimicrobial; antiparkinsonian; cancer;  
KW immune system disorder; angiogenesis; hyperproliferative disorder;  
KW cardiovascular disorder; apoptosis; hyperproliferative disease;  
KW infectious disease; wound healing.  
XX OS Homo sapiens.  
XX PN WO200035937-A1.  
XX PD 22-JUN-2000.  
XX PF 16-DEC-1999; 99WO-US029950.  
XX PR 17-DEC-1998; 98US-0112809P.  
XX PR 18-DEC-1998; 98US-0113006P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Ruben SM, Ebner R, Rosen CA, Endress GA, Soppet DR, Ni J;  
PI Duan DR, Moore PA, Shi Y, Lafleur DW, Olsen HS, Florence K;  
XX WPI; 2000-431566/37.  
XX PT Forty seven human nucleic acids encoding secreted proteins, useful in the  
PT treatment, prevention and diagnosis of cancers, disorders of the immune  
PT system, angiogenesis disorders, neurological diseases and  
PT hyperproliferative disorders.  
XX PS Disclosure; Page 37; 562pp; English.  
XX CC The polynucleotide sequence given in AAA78381 to AAA78432 encode the  
CC human secreted proteins given in AAB24437 to AAB24604. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: cytostatic; antianaemic;  
CC antidiabetic; antiinflammatory; ophthalmological; antirheumatic;  
CC antiarthritic; antipsoriatic; antiangiogenic; cardiant; anti-HIV;  
CC nootropic; neuroprotective; antimicrobial and antiparkinsonian. Human  
CC secreted protein polynucleotides, polypeptides, antagonists and/or  
CC agonists may be useful in treating, preventing, and/or diagnosing other  
CC diseases, disorders, and/or conditions such as: (a) cancers; (b)  
CC disorders of the immune system; (c) angiogenesis disorders; (d)  
CC hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases  
CC associated with increase apoptosis; (g) neurological diseases; and (h)  
CC infectious diseases. They are also used to promote wound healing.  
CC AAA78372 to AAA78380 and AAB24436 represent sequences used in the  
CC exemplification of the present invention  
XX SQ Sequence 442 AA;

Query Match 57.1%; Score 216; DB 3; Length 442;

Best Local Similarity 61.4%; Pred. No. 6.8e-19;  
Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;  
QY 2 LHFIDQHRRAALIAVTNNVWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSTPAWNW 61  
Db 339 LHFVDQYREQIARVTSVEVLDKLGQVLSQEQYERVLAEPTNPSQMRKLFSLQSQWDR 398  
QY 62 TCKDLLLQAL 71  
Db 399 KCKDGLYQAL 408

Search completed: July 28, 2004, 08:53:00  
Job time : 41.0602 secs







; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 195  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-340-620A-49

Query Match 100.0%; Score 378; DB 4; Length 195;  
Best Local Similarity 100.0%; Pred. No. 5.4e-42;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQRAALIAIARVTNVVWLLDALYGVLTDEQYQAVRAEPTNPCKMKLFSFTPAWN 60  
Db 111 GLHFDQRAALIAIARVTNVVWLLDALYGVLTDEQYQAVRAEPTNPCKMKLFSFTPAWN 170  
QY 61 WTCXDLLLQAL 71  
Db 171 WTCXDLLLQAL 181

## RESULT 3

US-09-340-620A-57  
; Sequence 57, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-340-620A-57

Query Match 69.8%; Score 264; DB 4; Length 70;  
Best Local Similarity 73.9%; Pred. No. 1.6e-27;  
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAIARVTNVVWLLDALYGVLTDEQYQAVRAEPTNPCKMKLFSFTPAWNWT 62  
Db 2 HFVDQHQALIAIARVTNVVWLLDALHGSVLTGQYQAVRAETTSQDKMKLFSFVPSWNL 61  
QY 63 CKDLLLQAL 71  
Db 62 CKDLLLQAL 70

## RESULT 4

US-09-340-620A-66  
; Sequence 66, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-340-620A-66

Query Match 69.8%; Score 264; DB 4; Length 70;  
Best Local Similarity 73.9%; Pred. No. 1.6e-27;  
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAIARVTNVVWLLDALYGVLTDEQYQAVRAEPTNPCKMKLFSFTPAWNWT 62  
Db 2 HFVDQHQALIAIARVTNVVWLLDALHGSVLTGQYQAVRAETTSQDKMKLFSFVPSWNL 61  
QY 63 CKDLLLQAL 71  
Db 62 CKDLLLQAL 70

## RESULT 5

US-09-340-620A-61  
; Sequence 61, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-340-620A-61

Query Match 69.8%; Score 264; DB 4; Length 193;  
Best Local Similarity 73.9%; Pred. No. 5.7e-27;  
Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 3 HFIDQRAALIAIARVTNVVWLLDALYGVLTDEQYQAVRAEPTNPCKMKLFSFTPAWNWT 62  
Db 111 HFVDQHQALIAIARVTNVVWLLDALHGSVLTGQYQAVRAETTSQDKMKLFSFVPSWNL 170  
QY 63 CKDLLLQAL 71  
Db 171 CKDLLLQAL 179

## RESULT 6

US-09-340-620A-71  
; Sequence 71, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(109)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-340-620A-71  
  
Query Match 34.5%; Score 130.5; DB 4; Length 109;  
Best Local Similarity 47.4%; Pred. No. 1.1e-09;  
Matches 37; Conservative 10; Mismatches 24; Indels 7; Gaps 4;  
  
QY 1 GLHFIDQHRALRIARVTN--VEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP 57  
Db 7 GSEIIDQHRALRIARVTEDPXDLSLLDALLSRDLISEEDYEAETTXLSKVRKLLILVQ 66  
  
QY 58 A-WNWTCKDL---LLQLAL 71  
Db 67 SKGEETCKFLKCLLOAL 84  
  
RESULT 7  
US-09-069-023-10  
; Sequence 10, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-10  
  
Query Match 18.4%; Score 69.5; DB 4; Length 106;  
Best Local Similarity 26.8%; Pred. No. 0.12;  
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
  
QY 5 IDQHRALRIARV-TNVEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP----- 56  
Db 12 IDREKRLVETLQADSGLLDALLARGVLTGPEYALDPAERRVRLLLLVQKGGA 71  
  
QY 57 -----PANW 61

Db 72 ACQELLRCQAORTAGAPDPADW 93  
|||:|  
RESULT 8  
US-09-069-023-8  
; Sequence 8, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 208  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-069-023-8  
  
Query Match 18.4%; Score 69.5; DB 4; Length 208;  
Best Local Similarity 26.8%; Pred. No. 0.28;  
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
  
QY 5 IDQHRALRIARV-TNVEWLLDALYK-VLTDEQYQAVRAEPTNPSKMKLFSTFP----- 56  
Db 12 IDREKRLVETLQADSGLLDALLARGVLTGPEYALDPAERRVRLLLLVQKGGA 71  
  
QY 57 -----PANW 61  
Db 72 ACQELLRCQAORTAGAPDPADW 93  
|||:|  
RESULT 9  
US-09-069-023-22  
; Sequence 22, Application US/09069023A  
; Patent No. 6348573  
; GENERAL INFORMATION:  
; APPLICANT: Nunez, Gabriel  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koseki, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
; FILE REFERENCE: UM-03333  
; CURRENT APPLICATION NUMBER: US/09/069,023A  
; CURRENT FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-069-023-22  
  
Query Match 18.4%; Score 69.5; DB 4; Length 221;  
Best Local Similarity 26.8%; Pred. No. 0.3;  
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
  
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Db 12 IDREKRLVETLQADSGLLDALLARGVLTGPEYALDPAERRVRLLLLVQKGGA 71  
  
QY 57 -----PANW 61  
Db 72 ACQELLRCQAORTVSMFPDPAW 93  
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RESULT 10

US-09-099-041A-31  
; Sequence 31, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-099-041A-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;  
Best Local Similarity 25.9%; Pred. No. 0.34;  
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
QY 6 DQRAALIAIV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT----- 56  
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRRLILLVQKGGEAA 69  
QY 57 -----PAWNW 61  
Db 70 CQELLRCQAQTAGAPDPANDW 90

RESULT 11  
US-09-245-281-31  
; Sequence 31, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-245-281-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;  
Best Local Similarity 25.9%; Pred. No. 0.34;  
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
QY 6 DQRAALIAIV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT----- 56  
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRRLILLVQKGGEAA 69  
QY 57 -----PAWNW 61  
Db 70 CQELLRCQAQTAGAPDPANDW 90

RESULT 12  
US-09-207-359B-31

; Sequence 31, Application US/09207359B  
; Patent No. 6469140  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-112001  
; CURRENT APPLICATION NUMBER: US/09/207,359B  
; CURRENT FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-207-359B-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;  
Best Local Similarity 25.9%; Pred. No. 0.34;  
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
QY 6 DQRAALIAIV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT----- 56  
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRRLILLVQKGGEAA 69  
QY 57 -----PAWNW 61  
Db 70 CQELLRCQAQTAGAPDPANDW 90

RESULT 13  
US-09-340-620A-31  
; Sequence 31, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-340-620A-31

Query Match 17.3%; Score 65.5; DB 4; Length 94;  
Best Local Similarity 25.9%; Pred. No. 0.34;  
Matches 21; Conservative 12; Mismatches 23; Indels 25; Gaps 3;  
QY 6 DQRAALIAIV-TNVEWLLDALYCK-VLTDEQYQAVRAEPTNPSKMKLFSFT----- 56  
Db 10 DRERKRLVETLQADSGLLLDALLARGVLTGPEYEALDLPDAERRVRRLILLVQKGGEAA 69  
QY 57 -----PAWNW 61  
Db 70 CQELLRCQAQTAGAPDPANDW 90

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Job time : 12.4036 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:54:53 ; Search time 34.6446 Seconds

(without alignments)  
642.856 Million cell updates/sec

Title: US-09-996-617-8\_COPY\_111\_181

Perfect score: 378

Sequence: 1 GLHFIDQHRAALIVTNVE.....LFSFTPMWTKDLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	71	9	US-09-728-721-58
2	378	100.0	71	14	US-10-295-981-58
3	378	100.0	85	9	US-09-841-879B-8
4	378	100.0	85	16	US-10-756-097-8
5	378	100.0	90	9	US-09-931-071-7
6	378	100.0	195	9	US-09-728-721-49
7	378	100.0	195	9	US-09-986-617-8
8	378	100.0	195	9	US-09-841-879B-5
9	378	100.0	195	12	US-10-446-046-4
10	378	100.0	195	14	US-10-295-981-49
11	378	100.0	195	15	US-10-240-145-55
12	378	100.0	195	15	US-10-131-410-84
13	378	100.0	195	16	US-10-756-097-5
14	378	100.0	205	14	US-10-106-698-5421
15	269	71.2	85	9	US-09-841-879B-15

16	269	71.2	85	16	US-10-756-097-15	Sequence 15, Appl
17	264	69.8	70	9	US-09-728-721-57	Sequence 57, Appl
18	264	69.8	70	9	US-09-728-721-66	Sequence 66, Appl
19	264	69.8	70	14	US-10-295-981-57	Sequence 57, Appl
20	264	69.8	70	14	US-10-295-981-66	Sequence 66, Appl
21	264	69.8	84	9	US-09-841-879B-7	Sequence 7, Appl
22	264	69.8	84	16	US-10-756-097-7	Sequence 7, Appl
23	264	69.8	193	9	US-09-728-721-61	Sequence 61, Appl
24	264	69.8	193	9	US-09-841-879B-2	Sequence 2, Appl
25	264	69.8	193	14	US-10-295-981-61	Sequence 61, Appl
26	264	69.8	193	16	US-10-756-097-2	Sequence 2, Appl
27	216	57.1	88	9	US-09-841-739-15	Sequence 15, Appl
28	216	57.1	88	14	US-10-449-315-15	Sequence 15, Appl
29	216	57.1	442	10	US-09-895-298-139	Sequence 139, Appl
30	216	57.1	1399	9	US-09-388-221-4	Sequence 4, Appl
31	216	57.1	1429	9	US-09-996-617-2	Sequence 2, Appl
32	216	57.1	1429	9	US-09-931-071-2	Sequence 3, Appl
33	216	57.1	1429	12	US-10-029-347-3	Sequence 26, Appl
34	216	57.1	1429	12	US-10-029-347-26	Sequence 11, Appl
35	216	57.1	1429	14	US-10-028-392-11	Sequence 3, Appl
36	216	57.1	1429	14	US-10-028-374-3	Sequence 15, Appl
37	216	57.1	1429	14	US-10-183-770-3	Sequence 15, Appl
38	216	57.1	1429	14	US-10-183-770-15	Sequence 6, Appl
39	216	57.1	1429	14	US-09-388-221-6	Sequence 2, Appl
40	216	57.1	1443	9	US-09-388-221-2	Sequence 8, Appl
41	216	57.1	1473	12	US-10-182-822A-8	Sequence 5422, Ap
42	216	57.1	1473	12	US-10-106-698-5422	Sequence 1120, Ap
43	214	56.6	158	14	US-10-106-698-5422	Sequence 145, App
44	214	56.6	190	9	US-09-925-301-1120	
45	141	37.3	65	10	US-09-895-298-145	

#### ALIGNMENTS

RESULT 1  
US-09-728-721-58  
; Sequence 59, Application US/09728721  
; Patent No US20020061845A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/728,721  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/340,620  
; PRIOR FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58  
; LENGTH: 71  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-728-721-58

Query Match 100.0%; Score 378; DB 9; Length 71;  
Best Local Similarity 100.0%; Pred. No. 5.6e-40;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIVTNVEWLLDLYGKVLDEQYQAVRAEPTNPSKMKLFSFTPAWN 60  
DB 1 GLHFIDQHRAALIVTNVEWLLDLYGKVLDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

QY 61 WTCKDLLQAL 71  
DB 61 WTCKDLLQAL 71

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RESULT 2
US-10-295-981-58
; Sequence 8, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-58

Query Match      100.0%; Score 378; DB 14; Length 71;
Best Local Similarity 100.0%; Pred. No. 5.6e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 3
US-09-841-879B-8
; Sequence 8, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/09/841,879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-879B-8

Query Match      100.0%; Score 378; DB 9; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 4
US-10-756-097-8
; Sequence 8, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-097-8

Query Match      100.0%; Score 378; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 5
US-09-931-071-7
; Sequence 7, Application US/09931071
; Patent No. US20020128219A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-335001
; CURRENT APPLICATION NUMBER: US/09/931,071
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/428,252
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-071-7

Query Match      100.0%; Score 378; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.4e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
DB 6 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 65
QY 61 WTCKDLLLQAL 71
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Db 61 WTCKDLLLQAL 71

RESULT 4
US-10-756-097-8
; Sequence 8, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-097-8

Query Match      100.0%; Score 378; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 6.9e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
DB 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
QY 61 WTCKDLLLQAL 71
DB 61 WTCKDLLLQAL 71

RESULT 5
US-09-931-071-7
; Sequence 7, Application US/09931071
; Patent No. US20020128219A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-335001
; CURRENT APPLICATION NUMBER: US/09/931,071
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/428,252
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-071-7

Query Match      100.0%; Score 378; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.4e-40;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 60
DB 6 GLHFDQHRALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSPKMKLFSFTPAWN 65
QY 61 WTCKDLLLQAL 71
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Db 66 WTCKDLLLQAL 76  
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## RESULT 6

US-09-728-721-49

; Sequence 49, Application US/09728721

; Patent No. US20020061845A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-124001

; CURRENT APPLICATION NUMBER: US/09/728,721

; CURRENT FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: 09/340,620

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: US 09/207,359

; PRIOR FILING DATE: 1998-12-08

; PRIOR APPLICATION NUMBER: US 09/099,041

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-728-721-49

Query Match 100.0%; Score 378; DB 9; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1.8e-39;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

QY 61 WTCKDLLLQAL 71

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Db 171 WTCKDLLLQAL 181

## RESULT 7

US-09-996-617-8

; Sequence 8, Application US/09996617

; Patent No. US20020128198A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-340001

; CURRENT APPLICATION NUMBER: US/09/996,617

; CURRENT FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 09/931,071

; PRIOR FILING DATE: 2001-08-15

; PRIOR APPLICATION NUMBER: 09/428,252

; PRIOR FILING DATE: 1999-10-27

; PRIOR APPLICATION NUMBER: 09/340,620

; PRIOR FILING DATE: 1999-06-28

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-617-8

Query Match 100.0%; Score 378; DB 9; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1.8e-39;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170  
|||||  
QY 61 WTCKDLLLQAL 71  
|||||  
Db 171 WTCKDLLLQAL 181  
|||||

## RESULT 8

US-09-841-879B-5

; Sequence 5, Application US/09841879B

; Patent No. US20020142979A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-330001

; CURRENT APPLICATION NUMBER: US/09/841,879B

; CURRENT FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 09/728,721

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: US 09/340,620

; PRIOR FILING DATE: 1999-06-28

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-841-879B-5

Query Match 100.0%; Score 378; DB 9; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1.8e-39;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

QY 61 WTCKDLLLQAL 71

|||||

Db 171 WTCKDLLLQAL 181

## RESULT 9

US-10-446-046-4

; Sequence 4, Application US/10446046

; Publication No. US20030224438A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; APPLICANT: Millennium Pharmaceuticals, Inc.

; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR

; FILE REFERENCE: MPI02-081P1RM

; CURRENT APPLICATION NUMBER: US/10/446,046

; CURRENT FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: 60/383487

; PRIOR FILING DATE: 2002-05-24

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-446-046-4

Query Match 100.0%; Score 378; DB 12; Length 195;  
Best Local Similarity 100.0%; Pred. No. 1.8e-39;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60

Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170

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QY 61 WTCKDLLOAL 71
Db 171 WTCKDLLOAL 181

RESULT 10
US-10-295-981-49
; Sequence 49, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-49

Query Match 100.0%; Score 378; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170

QY 61 WTCKDLLOAL 71
Db 171 WTCKDLLOAL 181

RESULT 11
US-10-240-145-55
; Sequence 55, Application US/10240145
; Publication No. US20030235883A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-048
; CURRENT APPLICATION NUMBER: US/10/240,145
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 55
; LENGTH: 195
; TYPE: PRT
US-10-240-145-55

Query Match 100.0%; Score 378; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170

QY 61 WTCKDLLOAL 71
Db 171 WTCKDLLOAL 181

RESULT 12
US-10-131-410-84
; Sequence 84, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERNI
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-84

Query Match 100.0%; Score 378; DB 15; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170

QY 61 WTCKDLLOAL 71
Db 171 WTCKDLLOAL 181

RESULT 13
US-10-756-097-5
; Sequence 5, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
```

```
; ORGANISM: Homo sapiens
US-10-240-145-55

Query Match 100.0%; Score 378; DB 15; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170

QY 61 WTCKDLLOAL 71
Db 171 WTCKDLLOAL 181
```

```
RESULT 12
US-10-131-410-84
; Sequence 84, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERNI
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-84
```

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Query Match 100.0%; Score 378; DB 15; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSTPAWN 170

QY 61 WTCKDLLOAL 71
Db 171 WTCKDLLOAL 181
```

```
RESULT 13
US-10-756-097-5
; Sequence 5, Application US/10756097
; Publication No. US20040127685A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/10/756,097
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: US/09/841,879B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
```

```
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-097-5

Query Match      100.0%; Score 378; DB 16; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Db 111 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 170
Qy 61 WTCKDLLLQAL 71
Db 171 WTCKDLLLQAL 181

RESULT 14
US-10-106-698-5421
; Sequence 5421, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5421
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5421

Query Match      100.0%; Score 378; DB 14; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.9e-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Db 121 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 180
Qy 61 WTCKDLLLQAL 71
Db 181 WTCKDLLLQAL 191

RESULT 15
US-09-841-879B-15
; Sequence 15, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/09/841.879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
```

```
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; NAME/KEY: VARIANT
; LOCATION: 2, 5, 18, 20, 21, 29, 34, 45-47, 56, 61, 67, 72, 74-75, 84
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-879B-15

Query Match      71.2%; Score 269; DB 9; Length 85;
Best Local Similarity 76.1%; Pred. No. 4.1e-26;
Matches 54; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GLHFIDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Db 1 GXHFYDQHRAALIAIARVTNVWLLDALYGVLTDEQYQAVRAEPTNPSKMKLFSFTPAWN 60
Qy 61 WTCKDLLLQAL 71
Db 61 WTCKDLLLQAL 71

Search completed: July 28, 2004, 09:04:14
Job time : 34.6446 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

QM protein - protein search, using sw model

Run on: July 28, 2004, 08:50:22 ; Search time 10.2651 seconds

(without alignments)  
665.325 Million cell updates/sec

Title: US-09-996-617-8\_COPY\_111\_181

Perfect score: 378

Sequence: 1 GLHFIDQRAALIAITVNE.....LFSFTPAWNTCKDLLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	216	57.1	1192	2 T17255	hypothetical prote
2	69.5	18.4	221	2 S70009	glutamate/proline-
3	68	18.0	545	2 A87136	hypothetical prote
4	64.5	17.1	605	2 T04197	hypothetical prote
5	64	16.9	304	2 G81417	cytochrome-c perox
6	62.5	16.5	211	2 S57940	YggA protein homol
7	62	16.4	779	2 A82402	alpha-glucosidase
8	61.5	16.3	306	2 T21132	hypothetical prote
9	61.5	16.3	346	2 A48470	translation elonga
10	61.5	16.3	1193	2 T21133	hypothetical prote
11	61	16.1	277	2 F83616	hypothetical prote
12	61	16.1	338	2 AF0294	probable lipote-p
13	61	16.1	345	2 T17608	probable GDPmannos
14	60.5	16.0	464	2 H82011	probable outer mem
15	60.5	16.0	724	2 C71274	hypothetical prote
16	60.5	16.0	877	2 JN0772	glucan endo-1,3-be
17	60	15.9	332	2 C83295	conserved hypothet
18	60	15.9	773	2 T39513	hypothetical prote
19	59.5	15.7	249	2 A35263	beta-lactamase (EC
20	59.5	15.7	290	2 I58425	arylamine N-acetyl
21	59	15.6	286	2 E82201	spermidine/putresc
22	59	15.6	371	2 S68072	major outer membra
23	59	15.6	381	2 E88427	protein R07E5.3 [i
24	59	15.6	529	2 S43599	Snf5 homolog R07E5
25	59	15.6	537	2 S62749	A-alpha X protein
26	59	15.6	542	2 D70873	probable ABC trans
27	59	15.6	681	2 E70942	hypothetical prote
28	59	15.6	1021	2 S09111	hypothetical prote
29	59	15.6	1023	2 G96509	protein F27F5.21 [

30 58.5 15.5 290 2 B61267  
31 58.5 15.5 368 2 T04861  
32 58.5 15.5 443 2 C75143  
33 58.5 15.5 498 2 AD0978  
34 58.5 15.5 554 2 S46346  
35 58.5 15.5 700 2 B82788  
36 58 15.3 192 2 A12271  
37 58 15.3 371 2 S68069  
38 57.5 15.2 156 2 AG3373  
39 57.5 15.2 280 2 F70943  
40 57.5 15.2 290 2 I67465  
41 57.5 15.2 350 2 B39364  
42 57.5 15.2 380 2 T29544  
43 57.5 15.2 446 2 S16308  
44 57.5 15.2 682 2 J00420  
45 57 15.1 233 2 S62063

arylamine N-acetyl  
hypothetical prote  
hypothetical prote  
L-xylokinase (EC  
Sag polyprotein -  
metalloproteinase X  
transcription regu  
major outer membra  
hypothetical prote  
hypothetical prote  
arylamine N-acetyl  
GBF-1 embryonic gr  
hypothetical prote  
translation elonga  
beta-1,3-glucanase  
H+-exporting ATPas

ALIGNMENTS

RESULT 1

T17255  
hypothetical protein DKFp586O1822.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T17255  
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A:Reference number: Z18722  
A:Accession: T17255  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1192 <KOE>  
A:Cross-references: EMBL:AL117470  
A:Experimental source: adult uterus; clone DKFp586O1822  
C:Genetics:  
A>Note: DKFp586O1822.1

Query Match 57.1%; Score 216; DB 2; Length 1192;

Best Local Similarity 61.4%; Pred. No. 6.1e-17;

Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 2 LHFIDQRAALIAITVNTVEVLDLALYGVLTDEQYQAVRAEPTNPSKMKLFSPFANW 61  
DB 1098 LHFVDQYREQLIARVTSVEVLDLKHGVLSQEQRVVAENTRPSQMKLFSLQSQWDR 1157  
QY 62 TCKDLLLQAL 71  
DB 1158 KCKDGLYQAL 1167

RESULT 2

S70009  
glutamate/proline-rich protein (clone 53.1.1.1) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S70009  
R:Geertman, R.; McMahon, A.; Sabban, E.L.  
Biochim. Biophys. Acta 1306, 147-152, 1996  
A:Title: Cloning and characterization of cDNAs for novel proteins with glutamic acid-pr  
A:Reference number: S70009; MUID:96221285; PMID:8634331  
A:Accession: S70009  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-221 <GEE>  
A:Cross-references: EMBL:U40627; NID:g1184693; PTDN:AAB05657.1; PID:g1184694

Query Match 18.4%; Score 69.5; DB 2; Length 221;

Best Local Similarity 26.8%; Pred. No. 1.3;

Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;

QY 5 IDQRAALIAIRV-TNVEVLDLALYGVLTDEQYQAVRAEPTNPSKMKLFSPF 56

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Db 12 IDRKRLVETLQADSGLLDALVARGVLTGPEYFALDPAERVRRLLLVQSKGEA 71
QY 57 -----PAWN 61
Db 72 ACQELLCAQQTVMSPDPDAWD 93

RESULT 3
A:7136
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: A87136
R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holt, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, R.; M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: A87136
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <STO>
A:Cross-references: GB:AL450380; NID:gl3093526; PIDN:CAC30769.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML1816
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 18.0%; Score 68; DB 2; Length 545;
Best Local Similarity 36.4%; Pred. No. 5.5;
Matches 20; Conservative 3; Mismatches 16; Indels 16; Gaps 2;

QY 5 HRAALIAVTNVEWLLDALYGVK-----LTDEYQAVRAEPTNSK 48
Db 226 HNELIAAVNRVWFLDAVLGKVDYVNGWYKYLDSRATDEQRR--RRRVNAER 278

RESULT 4
T04197
C:Species: Arabidopsis thaliana
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 28-Jul-2000
C:Accession: T04197
R: Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15260
A:Accession: T04197
A:Molecule type: DNA
A:Residues: 1-605 <BEV>
A:Cross-references: EMBL:AL049523
A:Experimental source: cultivar Columbia; BAC clone T4F9
C:Genetics:
A:Map position: 4
A:Introns: 415/3; 471/3
A:Note: T4F9.80
C:Superfamily: Arabidopsis thaliana hypothetical protein F2809.30

Query Match 17.1%; Score 64.5; DB 2; Length 605;
Best Local Similarity 30.6%; Pred. No. 16;
Matches 22; Conservative 11; Mismatches 30; Indels 9; Gaps 2;

QY 5 IDQHRAL-----IARVTNVEWLLDALYGVKLTDEYQAVRAEPTNSKRLKLPSP 55
Db 232 IDENNAWKEGSGNVRVWVVTIKDILPSSLPNRFQWVRLRAREGGLSKITLHFV 291
QY 56 TPANWNTCKDL 67
Db 292 SPVKNWGIKDLV 303

RESULT 5

```

```

G81417
C:cytochrome-c peroxidase (EC 1.1.1.1.5) Cj0020c [similarity] - Campylobacter jejuni (strain C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: G81417
R: Parkhill, J.; Wren, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chillin, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell, Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: G81417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-304 <PAR>
A:Cross-references: GB:AL139074; GB:AL111168; NID:G6967505; PIDN:CAB72513.1; PID:G696752
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0020c
C:Superfamily: Pseudomonas cytochrome-c peroxidase; Pseudomonas cytochrome-c peroxidase
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:56,59/Binding site: heme (Cys) (covalent) (low potential) #status predicted
F:60,259/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:199,202/Binding site: heme (Cys) (covalent) (high potential) #status predicted
F:203,273/Binding site: heme iron (His, Met) (axial ligands) (high potential) #status pr

Query Match 16.9%; Score 64; DB 2; Length 304;
Best Local Similarity 29.0%; Pred. No. 8.4;
Matches 20; Conservative 7; Mismatches 24; Indels 18; Gaps 3;

QY 3 HFIDQHRALIAVTNVEWLLDALYGVKLTDEYQAVRAEPTN-PSKVRKLPSPFPANW 61
Db 60 HRLDQHG-----VDGLFSGVDNQLD----KPFNTTTFNSVFNVFQFWNG 102
QY 62 TCKDILLQA 70
Db 103 RAKDLAEQA 111

RESULT 6
S57940
YGA protein homolog - Aeromonas hydrophila
C:Species: Aeromonas hydrophila
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C:Accession: S57940
R: Swift, S.; Fish, L.; Williams, P.; Stewart, G.S.A.B.
submitted to the EMBL Data Library, July 1995
A:Reference number: S57938
A:Accession: S57940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <SWI>
A:Cross-references: EMBL:X89469; NID:G899143; PIDN:CAA61655.1; PID:G899146

Query Match 16.5%; Score 62.5; DB 2; Length 211;
Best Local Similarity 24.6%; Pred. No. 8.3;
Matches 16; Conservative 11; Mismatches 33; Indels 5; Gaps 2;

QY 1 GLHFDQHRAL--IARVTNVEWLLDALYGVKLTDEYQAVRAEPTNPSKVRKLPSP 58
Db 123 GSCFAELRSAPAAVAMLASLWFWYSLAFAGVLPWLAGR---QGYSKLLILLVSPC 179
QY 59 WNWTC 63
Db 180 WGWRC 184

RESULT 7
AE2402
alpha-glucosidase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE2402

```



## RESULT 12

AF0294  
Probable lipopate-protein ligase A lpla [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AF0294  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0294  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-338 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CA051218.1; PID:g15980407; GSPDB:GN00175  
C:Genetics:  
A:Gene: lpla  
C:Superfamily: lipoate-protein ligase

Query Match 16.1%; Score 61; DB 2; Length 338;  
Best Local Similarity 32.3%; Pred. No. 21;  
Matches 21; Conservative 8; Mismatches 16; Indels 20; Gaps 4;

QY 14 ARVTNVEWLLDAL-YGKULT-----DEQYQVRAEPTNPSKMKLFSFT----- 56  
DB 183 SRVTNLVELFGIDHGKIRTAIEQAFYAYDEQ---VSAEIVSQSLPNLPGFTFEQFAKQ 239

QY 57 PAWNW 61

DB 240 SSNEW 244

## RESULT 13

T17608  
Probable GDPmannose 4,6-dehydratase (EC 4.2.1.47) - Chlorella virus PBCV-1  
N:Alternate names: GDP-D-mannose dehydratase  
C:Species: Chlorella virus PBCV-1  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T17608  
R:Graves, M.V.; Van Etten, J.L.  
Submitted to the EMBL Data Library, May 1999  
A:Reference number: Z18806  
A:Accession: T17608  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-345 <GRA>  
A:Cross-references: EMBL:U42580; NID:94028896; PIDN:AA096486.1  
A:Experimental source: specific host Chlorella strain NC64A  
C:Genetics:  
A:Note: A118R  
C:Superfamily: GDP-D-mannose dehydratase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 16.1%; Score 61; DB 2; Length 345;  
Best Local Similarity 28.6%; Pred. No. 22;  
Matches 22; Conservative 9; Mismatches 22; Indels 24; Gaps 3;

QY 8 HRAALIRV--TNVEWLDA-----LYGKVLTDQYQVRAEPTNPSK 48

DB 91 HQAEVTANVDALGVRLDVAIRAGLSNRICQASTSELYGKVLQEIPTERTFPYPSFYG 150

QY 49 MKLFSFTPAWNWTKD 65

DB 151 VAKLYAY-----WICKN 162

## RESULT 14

H82011  
Probable outer membrane protein NMA0178 [imported] - Neisseria meningitidis (strain Z249)  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001

C:Accession: H82011  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: H82011  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83493.1; PID:g737895  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA0178

Query Match 16.0%; Score 60.5; DB 2; Length 464;  
Best Local Similarity 25.7%; Pred. No. 35;  
Matches 18; Conservative 13; Mismatches 22; Indels 17; Gaps 2;

QY 10 AALIRVTNVEWLLDALYCKVLTDQYQVRAEPTNPSKMKL-----PSF 55

DB 173 AGIIAHTSAELRYKVDWGIM---EKALKETPPNPTAAQIKADGHADVKGSDWGFY 229

QY 56 TPAWNWTKD 65

DB 230 QLAWWDIND 239

## RESULT 15

C71274  
Hypothetical protein TP0851 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 24-Nov-1999  
C:Accession: C71274  
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwir,  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: C71274

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-724 <COL>

A:Cross-references: GB:AE001255; GB:AE000520; NID:g3323156; PIDN:AA065821.1; PID:g332316

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0851

C:Superfamily: syphilis spirochete hypothetical protein TP0851

Query Match 16.0%; Score 60.5; DB 2; Length 724;

Best Local Similarity 26.9%; Pred. No. 57;

Matches 21; Conservative 17; Mismatches 27; Indels 13; Gaps 5;

QY 3 HFIDQHRALIRVTNVEWLLDALYCK-VLTDEQYQAVR--AEPTNPSKMKLPSF---- 55

DB 132 YIIGHN--VILSRIDELCTNHAKEGAGLIKDGEQAEVRIIDPLNEITGGRKIFPFVGM 189

QY 56 -TPAWNWTC---KOLLQ 69

DB 190 AADAELWACHRDRTLLMQ 207

Search completed: July 28, 2004, 08:55:21

Job time : 12.2651 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2004, 08:46:37 ; Search time 6.84337 seconds  
(without alignments)  
540.228 Million cell updates/sec

Title: US-09-996-617-8\_COPY\_111\_181

Perfect score: 378

Sequence: 1 GLHFIDQRAALIRATVNE.....LFSFTPAWNWCKDLLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	100.0	195	1	Q9ulz3 homo sapien
2	264	69.8	193	1	Q9ebp4 mus musculus
3	216	57.1	1473	1	Q9c000 homo sapien
4	108	28.0	203	1	Q9i9n6 brachydanio
5	69.5	18.4	219	1	Q60936 homo sapien
6	69.5	18.4	220	1	Q60936 mus musculus
7	69.5	18.4	221	1	Q62881 rattus norv
8	68.5	18.1	431	1	Q9y2g2 homo sapien
9	67.5	17.9	539	1	P58801 mus musculus
10	66.5	17.6	611	1	Q90860 gallus gall
11	65	17.2	588	1	Q8k301 mus musculus
12	64.5	17.1	953	1	Q9y239 homo sapien
13	62.5	16.5	225	1	P52047 aeromonas h
14	62.5	16.5	540	1	Q43353 h receptor-
15	62	16.4	598	1	Q998t0 rattus norv
16	61.5	16.3	346	1	Q07051 eimeria bov
17	60.5	16.0	724	1	Q83823 treponema p
18	60	15.9	259	1	Q96p08 homo sapien
19	60	15.9	259	1	Q8vch9 mus musculus
20	60	15.9	332	1	Q9i048 pseudomonas
21	60	15.9	494	1	P79784 gallus gall
22	59.5	15.7	249	1	P25910 bacteroides
23	59.5	15.7	290	1	P50398 rattus norv
24	59.5	15.7	347	1	Q8r059 mus musculus
25	59	15.6	290	1	Q8k8u9 streptococc
26	59	15.6	371	1	P46027 haemophilus
27	59	15.6	1021	1	P16425 drosophila
28	58.5	15.5	290	1	P50295 mus musculus
29	58.5	15.5	612	1	Q62210 mus musculus
30	58.5	15.5	953	1	Q8bb0 mus musculus
31	58	15.3	117	1	Q32723 bacillus sp
32	57.5	15.2	290	1	P50297 rattus norv
33	57.5	15.2	350	1	P27545 mus musculus

34 57.5 15.2 446 1 ERIA\_STYLE  
35 57.5 15.2 682 1 E13B\_BACCI  
36 57.5 15.2 721 1 MASZ\_RHILO  
37 57 15.1 233 1 VATE\_YEAST  
38 57 15.1 375 1 YRFF\_VIBCH  
39 57 15.1 508 1 MML9\_HUMAN  
40 56.5 14.9 290 1 ARV1\_HUMAN  
41 56.5 14.9 347 1 GALE\_RAT  
42 56.5 14.9 463 1 EF11\_XENLA  
43 56.5 14.9 609 1 YL15\_MYCTA  
44 56.5 14.9 621 1 FX21\_HUMAN  
45 56.5 14.9 1634 1 PK3B\_HUMAN

#### ALIGNMENTS

RESULT 1  
ASC\_HUMAN  
ID ASC\_HUMAN STANDARD; PRT; 195 AA.  
AC Q9ULZ3; Q96D12; Q9BSZ5; Q9HBD0; Q9NXJ8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Apoptosis-associated speck-like protein containing a CARD (hASC)  
DE (PYCARD) (target of methylation-induced silencing 1) (Caspase  
DE recruitment domain protein 5).  
GN ASC OR TMS1 OR CARD5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Leukemia;  
RX MEDLINE=20036508; PubMed=10567338;  
RA Masumoto J., Hatanouchi S., Ayukawa K., Sarvotherm H., Kishino T.,  
RA Niihawa N., Hadaoka E., Katsuyama T., Higuchi T., Sagara J.;  
RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human  
RT promyelocytic leukemia HL-60 cells.";  
J. Biol. Chem. 274:33835-33838(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Fibroblast;  
RX MEDLINE=20552139; PubMed=1103776;  
RA Conway K.E., McConnell B.B., Bowring C.E., Donald C.D., Warren S.T.,  
RA Vertino P.M.;  
RT "TMS1, a novel proapoptotic caspase recruitment domain protein, is a  
RT target of methylation-induced gene silencing in human breast  
RT cancers.";  
Cancer Res. 60:6236-6242(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Martinon F., Hofmann K., Tschopp J.;  
RT "PYCARD a PYD and CARD containing molecule.";  
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Bertin J.;  
RT "CARD5 protein is a CARD/PYRIN family member that is involved in  
RT apoptosis signal transduction.";  
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Colon mucosa;  
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,  
RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,  
RA Nakamura Y., Isogai T., Sugano S.;  
RT "NEDD human cDNA sequencing project.";  
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
RC TISSUE=Lymph. and Pancreas;

RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Richardson S., Muzly D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP FUNCTION, AND SUBCELLULAR LOCATION.  
 RX MEDLINE=20552140; PubMed=11103777;  
 RA McConnell B.B., Vertino P.M.;  
 RT "Activation of a caspase-9-mediated apoptotic pathway by subcellular  
 RT redistribution of the novel caspase recruitment domain protein TMS1.";  
 RL Cancer Res. 60:6243-6247(2000).  
 CC -!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic  
 CC activity is mediated predominantly through the activation of  
 CC caspase 9.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation,  
 CC a redistribution from the cytoplasm to the aggregates occurs.  
 CC These appeared as hollow, perinuclear spherical, ball-like  
 CC structures.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=Q9ULZ3-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9ULZ3-2; Sequence=VSP\_004119;  
 CC Name=3;  
 CC IsoId=Q9ULZ3-3; Sequence=VSP\_004118;  
 CC Note-No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Widely expressed at low levels. Detected in  
 CC peripheral blood leukocytes, lung, small intestine, spleen,  
 CC thymus, colon and at lower levels in placenta, liver and kidney.  
 CC Very low expression in skeletal muscle, heart and brain. Detected  
 CC in the leukemia cell lines HL-60 and U937, but not in Jurkat T-  
 CC cell lymphoma and Daudi Burkitt's lymphoma. Detected in the  
 CC melanoma cell line WM35, but not in WM793. Not detected in HeLa  
 CC cervical carcinoma cells and Molt 4 lymphocytic leukemia cells.  
 CC -!- MISCELLANEOUS: In breast tumorigenesis, methylation-mediated  
 CC silencing may affect genes and proteins that act as positive  
 CC mediators of cell death.  
 CC -!- SIMILARITY: Contains 1 DAPIN domain.  
 CC -!- SIMILARITY: Contains 1 CARD domain.  
 CC -!- CAUTION: Ref.5 sequence differs from that shown due to a  
 CC frameshift in position 4.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [licenses@isb-sib.ch](mailto:licenses@isb-sib.ch)).  
 CC -----  
 CC EMBL; AB023416; BAA97339.2;  
 CC EMBL; AF184072; AAG01187.1;  
 CC EMBL; AF184073; AAG01188.1;  
 CC EMBL; AF255794; AAF99665.1;  
 CC EMBL; AF310103; AAG30286.1;  
 CC -----

DR EMBL; AF384665; AAK63850.1;  
 DR EMBL; AK000211; BAA91012.1; ALT\_FRAME.  
 DR EMBL; BC004470; AAH04470.1;  
 DR EMBL; BC013569; AAH13569.1; ALT\_INIT.  
 DR MIM; 606838;  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR InterPro; IPR001315; CARD.  
 DR InterPro; IPR004020; PAAD DAPIN\_dom.  
 DR Pfam; PF02758; PAAD DAPIN; 1.  
 DR PROSITE; PS02009; CARD; 1.  
 DR PROSITE; PS0824; DAPIN; 1.  
 KW Apoptosis; Anti-oncogene; Alternative splicing.  
 FT DOMAIN 1 91  
 FT CARD.  
 FT VARSPLIC 26 85  
 FT Missing (in isoform 3).  
 FT VARSPLIC 93 111  
 FT Missing (in isoform 2).  
 FT /FTID=VSP\_004119.  
 SQ SEQUENCE 195 AA; 21627 MW; 455987286586F46A CRC64;  
 Query Match 100.0%; Score 378; DB 1; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-37;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLHFDQHRRAALIARVTNVEWLLDLYGKVLTDQYQAVRAEPTNPSCVRKLFSTPAWN 60  
 DB 111 GLHFDQHRRAALIARVTNVEWLLDLYGKVLTDQYQAVRAEPTNPSCVRKLFSTPAWN 170  
 QY 61 WTCKDLILQAL 71  
 DB 171 WTCKDLILQAL 181  
 RESULT 2  
 ASC\_MOUSE  
 ID\_ASC\_MOUSE STANDARD; PRT; 193 AA.  
 AC Q9E8B4; Q9D2W9; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Apoptosis-associated speck-like protein containing a CARD (nASC)  
 DE (PYCARD).  
 GN ASC.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Thymus;  
 RX MEDLINE=20580347; PubMed=11139337;  
 RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagawa J.;  
 RT "Murine ortholog of ASC, a CARD-containing protein, self-associates  
 RT and exhibits restricted distribution in developing mouse embryos.";  
 RL Exp. Cell Res. 262:128-133(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Breast tumor;  
 RA Martinon F., Hofmann K., Tschopp J.;  
 RT "Pycard a PYD and CARD containing molecule.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Tongue;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayaashizaki Y.,  
"Functional annotation of a full-length mouse cDNA collection.";  
Nature 409:685-690(2001).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=22388257; PubMed=12477932;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin I.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J.J., Helton E., Ketterman M., Maman A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:15699-15903(2002).  
-!- FUNCTION: Promotes caspase-mediated apoptosis. This proapoptotic activity is mediated predominantly through the activation of caspase 9 (By similarity).  
-!- SUBCELLULAR LOCATION: Cytoplasmic. Upstream of caspase activation, a redistribution from the cytoplasm to the aggregates occurs. These appeared as hollow, perinuclear spherical, ball-like structures (By similarity).  
-!- TISSUE SPECIFICITY: Expressed in small intestine, colon, thymus, spleen, brain, heart, skeletal muscle, kidney, lung and liver.  
-!- DEVELOPMENTAL STAGE: Strongly expressed at E9.5 day in the telencephalon, thalamic areas of the diencephalon, heart and liver.  
-!- SIMILARITY: Contains 1 DAPIN domain.  
-!- SIMILARITY: Contains 1 CARD domain.  
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-----  
EMBL; AB032249; BAB16609.1; -  
EMBL; AF310104; AAG30287.1; -  
EMBL; AK009852; BAB26543.1; -  
EMBL; AK007742; BAB25229.1; -  
EMBL; AK019682; BAB31341.1; -  
EMBL; BC008252; AAR08252.1; -  
MGD; MGI:1931465; Asc.  
GO; GO:0005829; C:cytosol; IDA.  
InterPro; IPR001315; CARD.  
InterPro; IPR004020; PAAD\_DAPIN\_dom.  
Pfam; PF02758; PAAD\_DAPIN; 1.  
PROSITE; PS50309; CARD; 1.  
PROSITE; PS50824; DAPIN; 1.  
Apoptosis; Anti-oncogene.  
DOMAIN 1 91 DAPIN.  
KW FT

FT	DNAID_105		CARD.	
FT	CONFLICT	K -> E (IN REF. 3).		
SQ	SEQUENCE	193 AA;	21458 MW;	2A4EA40194870B31 CRC64;
 Query Match            69.8%; Score 264; DB 1; Length 193; Best Local Similarity 73.9%; Pred.No. 7.9e-24; Matches 51; Conservative 7; Mismatches 11; Indels 0; Gaps 0;				
QY	3 HFIDQHRAALIAVTNVVEMLLDALYGKVLTDGQQAVRAEPTNPSPMKRKLFSFPAWNT 62           :   :   :   :   :   :   :   :   :   :   :   :             :   :   :   :   :   :   :   :   :   :   :   :			
Db	111 HFFVDHQHQAALIAVTTEVDGVLDLHGSLVTLEGYQAVRAETTSQDKMRKLFSFPWSNLT 170           :   :   :   :   :   :   :   :   :   :   :   :             :   :   :   :   :   :   :   :   :   :   :   :			
QY	63 CKDILLICAL 71 			
Db	171 KOSLIQAL 179 			
 RESULT 3				
NALI_HUMAN		STANDARD;	PRT;	1473 AA.
ID_NALI_HUMAN		Q9C000; Q9BZ28; Q9BZZ9; Q9HAV8; Q9UFT4; Q9YZE0;		
AC	16-OCT-2001 (Rel. 40, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DE	NACT-, LRR- and PYD-containing protein 2 (Death effector filament-forming ced-4-like apoptosis protein) (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7). NALP1 OR DECAP OR CARD7 OR KIAA0926. NALP1 OR DECAP OR CARD7 OR KIAA0926.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=21169419; PubMed=11270363;			
RA	Bertin J., Disceano P.S.;			
RT	"the PYRN domain: a novel motif found in apoptosis and inflammation proteins.";			
RL	Cell Death Differ. 7:1273-1274(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=21148093; PubMed=11250163;			
RA	Martinson F., Hofmann K., Tschoopp J.;			
RT	"The pyrin domain: a possible member of the death domain-fold family implicated in apoptosis and inflammation.";			
RL	Curr. Biol. 11:R118-R120(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
TX	TISSUE=ErythroLeukemia;			
RC	MEDLINE=21153743; PubMed=11076957;			
RA	Hlaing T., Guo R.-F., Dillek A.A., Loussia J.M., Morrish T.A., Shi M.M., Vincenz C., Ward P.A.;			
RT	"Molecular cloning and characterization of DECAP-L and -S, two isoforms of a novel member of the mammalian Ced-4 family of apoptosis proteins.";			
RL	J. Biol. Chem. 276:9230-9238(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND PROTEIN INTERACTION.			
RC	TISSUE=T-cell;			
EX	MEDLINE=21153744; PubMed=1113115;			
RA	Chu Z.-L., Pio F., Xie Z., Welsh K., Krajewska M., Krajewski S., Godzik A., Reed J.C.;			
RT	"A novel enhancer of the Apaf1 apoptosome involved in cytochrome c-dependent caspase activation and apoptosis.";			
RL	J. Biol. Chem. 276:9239-9245(2001).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
TC	TISSUE=BRAIN;			
RC	MEDLINE=99246063; PubMed=10231032;			
RA	Ngase T.I., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code			

for large proteins in vitro.";  
DNA Res. 6:63-70(1999).  
[6]  
SEQUENCE OF 282-1473 FROM N.A. (ISOFORM 1).  
TISSUE=Uterus;  
Kohrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;  
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Able to form cytoplasmic structures termed death  
CC effector filaments. Enhances APAF1 and cytochrome c-dependent  
CC activation of pro-caspase-9 and consecutive apoptosis. Seems to  
CC bind ATP.  
CC  
CC -!- SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9  
CC and with APAF1 in a cytochrome c-inducible way leading to the  
CC formation of an apoptosome. This interaction may be ATP-dependent.  
CC  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing. Named isoforms=4;  
CC Name=1; Synonyms=NAC beta, DEFCAP-L;  
CC IsoId=Q9C000-1; Sequence=Displayed;  
CC Name=2; Synonyms=NAC alpha, DEFCAP-S;  
CC IsoId=Q9C000-2; Sequence=VSP\_004327;  
CC Name=3; Synonyms=NAC gamma;  
CC IsoId=Q9C000-3; Sequence=VSP\_004326, VSP\_004327;  
CC Name=4; Synonyms=NAC delta; Sequence=VSP\_004326;  
CC IsoId=Q9C000-4; Sequence=VSP\_004326;  
CC -!- TISSUE SPECIFICITY: Widely expressed. Isoforms 1 and 2 are  
CC expressed in peripheral blood leukocytes, chronic myelogenous  
CC leukemia cell line K-562, followed by thymus, spleen and heart.  
CC Also detected in lung, placenta, small intestine, colon, kidney,  
CC liver and muscle.  
CC  
CC -!- SIMILARITY: Contains 1 DAPIN domain.  
CC -!- SIMILARITY: Contains 1 NACHT domain.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.  
CC  
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CC  
CC EMBL; AF298548; AAG15254.1; -  
CC EMBL; AF310105; AAG30288.1; -  
CC EMBL; AF229059; AAK00748.1; -  
CC EMBL; AF229060; AAK00749.1; -  
CC EMBL; AF229061; AAK00750.1; -  
CC EMBL; AF229062; AAK00751.1; -  
CC EMBL; AB023143; BAA76770.1; -  
CC EMBL; AL117470; CAB55945.1; -  
CC PIR; T17255; T17255. -  
CC HSP; F13489; I44r. -  
CC MIM; 606636; -  
CC GO; GO:0005622; C:intracellular; IC.  
CC GO; GO:0016506; F:apoptosis activator activity; NAS.  
CC GO; GO:0008656; F:caspase activator activity; NAS.  
CC GO; GO:0019899; F:enzyme binding; IPI.  
CC GO; GO:0006919; P:caspase activation; NAS.  
CC GO; GO:0008917; P:induction of apoptosis; NAS.  
CC InterPro; IPR001315; CARD.  
CC InterPro; IPR000767; Disease\_resist.  
CC InterPro; IPR001611; LRR.  
CC InterPro; IPR007091; LRR\_RNinh.  
CC InterPro; IPR007111; NACHT\_Ntrase.  
CC InterPro; IPR004020; PAAD\_DAPIN\_dom.  
CC Pfam; PF00560; LRR; 2.  
CC Pfam; PF05729; NACHT; 1.  
CC Pfam; PF02758; PAAD\_DAPIN; 1.  
CC PRINTS; PR00364; DISEASERESIST.  
CC PROSITE; PS02029; CARD; 1.  
CC PROSITE; PS0824; DAPIN; 1.  
CC PROSITE; PS50837; NACHT; 1.

KW Apoptosis; ATP-binding; Leucine-rich repeat; Repeat;  
KW Alternative splicing.  
FT DOMAIN 1 92 DAPIN.  
FT DOMAIN 328 637 NACHT.  
FT LRR 1. 704 725  
FT REPEAT 807 830  
FT REPEAT 864 887  
FT REPEAT 921 944  
FT REPEAT 950 973  
FT REPEAT 1139 1215  
FT REPEAT 1216 1236  
FT REPEAT 1374 1463  
FT DOMAIN 334 341  
FT NP\_BIND 334 341  
FT VARSPPLIC 958 987  
FT VARSPPLIC 1262 1305  
FT MUTAGEN 340 340  
FT MUTAGEN 340 340  
FT CONFLICT 155 155  
FT CONFLICT 246 246  
FT CONFLICT 782 782  
FT CONFLICT 878 878  
FT CONFLICT 995 995  
FT CONFLICT 1119 1119  
FT CONFLICT 1184 1184  
FT CONFLICT 1241 1241  
FT CONFLICT 1366 1366  
FT CONFLICT 1473 AA; 165865 MW; 438F0DC45C2562D CRC64;  
SQ SEQUENCE 1473 AA; 57.1%; Score 216; DB 1; Length 1473;  
Query Match 57.1%; Score 216; DB 1; Length 1473;  
Best Local Similarity 61.4%; Pred. No. 3.1e-17;  
Matches 43; Conservative 12; Mismatches 15; Indels 0; Gaps 0;  
QY 2 LHFIDQRAALARTVNTVEWLDALYGVLTDEQYQAVAEPTNPSKMKLFSPFPAWNV 61  
DB 1379 LHFVDQYRQLIARTVSEVWLDLHGQVLSEQYERVLAEITRPSQMRKLFSLQSQWDR 1438  
QY 62 TCKDLQLLOAL 71  
DB 1439 KCKDGLYQAL 1448  
RESULT 4  
ASC BRARE STANDARD; PRT; 203 AA.  
ID ASC BRARE  
AC Q913N6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Apoptosis-associated speck-like protein containing a CARD (PYCARD).  
GN ASC OR ASC1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT Genes with homology to mammalian apoptosis regulators identified in  
RT Zebrafish.  
RL Cell Death Differ. 7:509-510(2000).  
CC -!- FUNCTION: Promotes caspase-mediated apoptosis (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Contains 1 DAPIN domain.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
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-----  
 DR EMBL; AF231013; AAF66956.1; -  
 DR ZFIN; ZDB-GENE-000511-2; ascl.  
 DR InterPro; IPR001315; CARD.  
 DR Pfam; PF02758; PAAD\_DAPIN\_dom.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS50824; DAPIN; 1.  
 DR Apoptosis; Anti-oncogene.  
 FT DOMAIN 1 91  
 FT DOWAIN 112 203  
 FT DOWAIN 112 203  
 SQ SEQUENCE 203 AA; 22867 MW; EF45179EB7A78A7 CRC64;

Query Match 28.0%; Score 106; DB 1; Length 203;  
 Best Local Similarity 42.5%; Pred. No. 3e+05;  
 Matches 31; Conservative 13; Mismatches 25; Indels 4; Gaps 3;

QY 2 LHFIDQRAALIAIVTVNEWLLDAL-YGKVLTDQYQAVRAEPTNPKMKLFS--FTPA 58  
 Db 117 VNFIDEHWKELIDRVNVDPLDILROKKVITNEDYCTIRKETPKQKRELITGPITCA 176  
 QY 59 WNWTCCKDLLOAL 71  
 Db 177 GN-KGKEVLYDAL 188

## RESULT 5

NOL3\_HUMAN  
 ID NOL3\_HUMAN STANDARD; PRT; 219 AA.  
 AC O60936; O60937;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Nucleolar protein 3 (apoptosis repressor with CARD) (Muscle-enriched  
 DE cytoplasmic protein) (Myp) (Nucleolar protein of 30 kDa) (Nop30).  
 GN NOL3 OR ARC OR NOP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=98226784; PubMed=9560245;  
 RA Koseki T., Inohara N., Chen S., Nunez G.;  
 RT "ARC, an inhibitor of apoptosis expressed in skeletal muscle and heart  
 RT that interacts selectively with caspases";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:5156-5160(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE=99214168; PubMed=10196175;  
 RA Stoss O., Schwaiger F.-W., Cooper T.A., Stamm S.;  
 RT "Alternative splicing determines the intracellular localization of the  
 RT novel nuclear protein Nop30 and its interaction with the splicing  
 RT factor SRS30c";  
 RL J. Biol. Chem. 274:10951-10962(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton B., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
 CC -!- FUNCTION: The nuclear isoform (1/Nop30) may be involved in RNA  
 CC splicing and the cytoplasmic isoform (2/Myp) may inhibit  
 CC apoptosis.  
 CC -!- SUBUNIT: Isoform 1 oligomerizes and binds to SRS9/SRP30C and also  
 CC interacts with NPM1. Isoform 2 binds caspase-2, caspase-8 and CED-  
 CC 3 and inhibits caspase-8 activity.  
 CC -!- SUBCELLULAR LOCATION: Nuclear or cytoplasmic. Isoform 1 is found  
 CC in nucleoli and nucleoplasm. Isoform 2 is cytoplasmic.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Nop30;  
 CC IsoId=O60936-1; Sequences=Displayed;  
 CC Name=2; Synonyms=Myp;  
 CC IsoId=O60936-2; Sequences=VSP 000789;  
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart and skeletal muscle.  
 CC Detected at low levels in placenta, liver, kidney and pancreas.  
 CC -!- SIMILARITY: Contains 1 CARD domain.  
 CC  
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EMBL; AF064599; AAC18593.1; -  
 DR EMBL; AF064600; AAC18594.1; -  
 DR EMBL; AF064598; AAC18590.1; -  
 DR EMBL; AF064598; AAC18591.1; -  
 DR EMBL; AF043244; AAC34993.1; -  
 DR EMBL; EC012798; AAH12798.1; -  
 DR Genew; HGNC:7869; NOL3.  
 DR GK; O60936; -  
 DR MIM; 605235; -  
 DR InterPro; IPR001315; CARD.  
 DR SMART; SM00114; CARD; 1.  
 DR PROSITE; PS50209; CARD; 1.  
 KW Apoptosis; Nuclear protein; mRNA splicing; Alternative splicing.  
 FT DOMAIN 4 95  
 FT VARSPLIC 96 219  
 FT CARD.  
 FT ATGTAATLHAQATGRRHRHARGHPAGCPPELQTLTRFPCAL  
 FT RAPRCNFGPRRSQSWKRLPLKRLNRSQSQSWNPRLK  
 FT QNQRNQNRTQSPSTSRKTSKIPKIPGQSSDRRCFAHA  
 FT G -> VGFYGRDRSDPPCGHWTPEAPSGTTCPLPRAH  
 FT DPDEAGGEGSEVQSGTPESEPELEAEASKEAPEPEPE  
 FT PELEPEAEPEPELEPEPEPEPEPEPEPEPEPEPEPE  
 FT Isoform 2).  
 FT /FTID=VSP\_000789.  
 SQ SEQUENCE 219 AA; 24327 MW; B1CCCB199D4FEE09 CRC64;

Query Match 18.4%; Score 69.5; DB 1; Length 219;  
 Best Local Similarity 26.8%; Pred. No. 0.63; 23; Indels 25; Gaps 3;  
 Matches 22; Conservative 12; Mismatches 12;  
 QY 5 IDQHPAALIAIV-TNVEWLLDALYK-VLTDEYQAVRAEPTNPKMKLFSFT----- 56  
 Db 12 IDREKRKLVTQLQADSGLLDALLARGVLTGVEYALDAPDAERVRLLLVQKGEA 71  
 QY 57 -----PANW 61  
 Db 72 AQCELLCAQRTAGAPDPANW 93

```

RESULT 7
NOL3_RAT
IID_NOL3_RAT STANDARD; PRT: 221 AA.
Q62881;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleolar protein 3.
NOL3.
Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Brain, and Pheochromocytoma;
MEDLINE=96221285; PubMed=8634331;
Geertman R., McMahon A., Sabban E.L.;
Cloning and characterization of cDNAs for novel proteins with
glutamic acid-proline dipeptide tandem repeats." ;
Biochim. Biophys. Acta 1308:147-152(1996).
Biol. FUNCTION: May be involved in RNA splicing (By similarity).
-! SUBUNIT: Interacts with Srp30c, NPML, CASP2, CASP8 and CED-3 (By
similarity).
-! SUBCELLULAR LOCATION: Nuclear (By similarity).
-! TISSUE SPECIFICITY: Highly expressed in skeletal muscle, heart and
medulla.
-! SIMILARITY: Contains 1 CARD domain.
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EMBL; U40627; AB05667.1; -.
PIR; S70009; S70009.
InterPro; IPR001315; CARD.
SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1.
Nuclear protein; mRNA splicing.
DOMAIN 4 95
FT DOMAIN 107 219
GLU/PRO-RICH.
SEQUENCE 221 AA; 24576 MW; A7661C9040B2CD4D CRC64;
Query Match 18.4%; Score 69.5; DB 1; Length 221;
Best Local Similarity 26.8%; Pred. No. 0.64;
Matches 22; Conservative 12; Mismatches 23; Indels 25; Gaps 3;
QY 5 IDQHRAALIARV-TNVVEILLDALYCK-VLTDSQYQAVRAEPTNPSSKVKLFST----- 56
|||::: : : : |||::: |||::: |||::: |||::: |||::: |||:::
Db 12 IDRERKRVLVETLQADSGLLLDNALVARGVLTGPYEYALDLPDAERRVRLLLLLVQSKGEA 71
||||: : : : |||::: |||::: |||::: |||::: |||::: |||:::
QY 57 -----PAWNW 61
||||:
Db 72 ACQELLRCQAQTVMSPDPAMDW 93
-----
RESULT 8
CAR8_HUMAN
IID CAR8_HUMAN STANDARD; PRT: 431 AA.
Q9Y2G2; Q96P82;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
DE DE Caspase recruitment domain protein 8 (Apoptotic protein NDPPL1) (DACAR)
GN (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (TUCAN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RC TISSUE=Brain;  
RX MEDLINE=99246063; PubMed=10231032;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XIII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:63-70(1999).  
RN [2]  
RN SEQUENCE FROM N.A. (ISOFORM LONG).  
RX MEDLINE=21950691; PubMed=11821383;  
RA Razmara M., Srinivasula S.M., Wang L., Poyet J.-L., Geddes B.J.,  
RA Disterhoop P.S., Bertin J., Alnemri E.S.;  
RT "CARD-8 protein, a new CARD family member that regulates caspase-1  
RT activation and apoptosis.";  
RL J. Biol. Chem. 277:13952-13958(2002).  
RN [3]  
RN SEQUENCE FROM N.A. (ISOFORM LONG).  
RX Zhang H.;  
RT "A novel apoptotic protein, NDP1, containing CARD and BH3 domains.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN SEQUENCE FROM N.A. (ISOFORM LONG).  
RX Guet C., Vito P.;  
RT "DACAR, a novel CARD-containing protein.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RN SEQUENCE FROM N.A. (ISOFORM LONG).  
RX MEDLINE=21570185; PubMed=11551959;  
RA Bouchier-Hayes L., Conroy H., Egan H., Adrain C., Creagh E.M.,  
RA MacFarlane M., Martin S.J.;  
RT "CARDINAL, a novel caspase recruitment domain protein, is an inhibitor  
RT of multiple NF-kappa B activation pathways.";  
RL J. Biol. Chem. 276:44069-44077(2001).  
RN [6]  
RN SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX T'SSUB=Kidney;  
RL Guo J.H., Yu L.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RN CHARACTERIZATION.  
RX MEDLINE=21402909; PubMed=11408476;  
RA Pathan N., Marusawa H., Krajewska M., Matsuzawa S.-I., Kim H.,  
RA Okada K., Torii S., Kitada S., Krajewski S., Welsh K., Pio F.,  
RA Godzik A., Reed J.C.;  
RT "TUCAN, an antiapoptotic caspase-associated recruitment domain family  
RT protein overexpressed in cancer.";  
RL J. Biol. Chem. 276:32220-32229(2001).  
RN [8]  
RN CHARACTERIZATION, AND MUTAGENESIS OF LEU-366.  
RX MEDLINE=22062958; PubMed=12067710;  
RA Stilo R., Leonardi A., Formisano L., Di Jeso B., Vito P., Liguoro D.;  
RT "TUCAN/CARDINAL and DRAL participate in a common pathway for  
RT modulation of NF-kappa B activation.";  
RL FEBS Lett. 521:165-169(2002).  
CC -!- FUNCTION: Inhibits NF-kappa-B activation. May participate in a  
CC regulatory mechanism that coordinates cellular responses  
CC controlled by NF-kappa-B transcription factor. Involved in the  
CC negative regulation of caspase-1.  
CC -!- SUBUNIT: May form homodimers. Interacts with NEMO and DRAL. Binds  
CC to caspase-1, pseudo-ICE and ICEBERG. Interacts with FNEP3 (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=Q9Y2G2-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=Q9Y2G2-2; Sequence=VSP\_000782, VSP\_000783;

CC -!- TISSUE SPECIFICITY: High expression in lung, ovary, testis and  
CC placenta. Lower expression in heart, kidney and liver. Also  
CC expressed in spleen, lymph node and bone marrow.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC  
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CC  
CC EMBL; AB023172; BAA76799.1; -;  
CC EMBL; AF322184; AAG50014.1; -;  
CC EMBL; AF331519; AAK01126.1; -;  
CC EMBL; AF026322; AAK08982.1; -;  
CC EMBL; AF405558; AAL02427.1; -;  
CC EMBL; AF511652; AAM46959.1; -;  
CC InterPro; IPR001315; CARD.  
CC Pfam; PF00619; CARD; 1.  
CC SMART; SM00114; CARD; 1.  
CC PROSITE; PS50209; CARD; 1.  
KW Apoptosis; Nuclear protein; Alternative splicing.  
FT DOMAIN 340 430  
FT VARSPLIC 282 286  
FT VARSPLIC 287 431  
FT MUTAGEN 366 366 L->R; INHIBITS HOMODIMER FORMATION.  
FT CONFLICT 60 60 E -> G (IN REF. 5).  
FT CONFLICT 326 326 V -> M (IN REF. 5).  
FT CONFLICT 422 422 L -> P (IN REF. 5).  
SQ SEQUENCE 431 AA; 48932 MW; CB54D130807732E6 CRC64;  
  
Query Match 18.1%; Score 68.5; DB 1; Length 431;  
Best Local Similarity 27.8%; Pred. No. 1.7; Mismatches 1; Gaps 1;  
Matches 20; Conservative 16;  
  
QY 1 GLHFTDQRAALIAIARVTVNEMLLDALY-GKVLTDQYQAVRAEPTNPKRKLFFSTPAW 59  
Db 344 GAAFKVENEHQALQARMGDLKGLVDLDQNEVLTEKELVEQETKQSKNEALLSWKVK 403  
QY 60 NWTCKDILLQAL 71  
Db 404 GDALDVLFRSI 415  
  
RESULT 9  
R1K2 MOUSE  
ID R1K2 MOUSE STANDARD; PRT; 539 AA.  
AC P58801;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37).  
GN R1K2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCB1\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=21891093; PubMed=11894097;  
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;  
RT "Involvement of receptor-interacting protein 2 in innate and adaptive  
RT immune responses.";  
RL Nature 416:190-194(2002).  
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CC CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SUBUNIT: Binds to CFLAR/CLARP and CASP1 via their CARD domains.

CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and  
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
CC receptor complex (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -!- PTM: Autophosphorylated (By similarity).  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC  
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CC  
CC EMBL; AF461040; AAL96436.1; -.  
CC MGD; MG1:1891456; Rlpk2.  
CC InterPro; IPR001315; CARD.  
CC InterPro; IPR000719; Prot\_kinase.  
CC InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
CC InterPro; IPR001245; Tyr\_pkinase.  
CC Pfam; PF00619; CARD; 1.  
CC Pfam; PF00069; pkinase; 1.  
CC PRINTS; PR00109; TYRKINASE.  
CC ProDom; PD000001; Prot\_kinase; 1.  
CC SMART; SM00114; CARD; 1.  
CC PROSITE; PS00209; CARD; 1.  
CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.  
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
CC Phosphorylation; Apoptosis.  
CC FT DOMAIN 18 294 PROTEIN KINASE.  
CC FT DOMAIN 431 523 CARD.  
CC FT NP\_BIND 24 32 ATP (BY SIMILARITY).  
CC FT BINDING 47 47 ATP (BY SIMILARITY).  
CC FT ACT\_SITE 146 146 BY SIMILARITY.  
CC SEQUENCE 539 AA; 60400 MW; 42951BF97CA15DFA CRC64;  
Query Match 17.9%; Score 67.5; DB 1; Length 539;  
Best Local Similarity 30.8%; Pred. No. 2.9;  
Matches 16; Conservative 15; Mismatches 18; Indels 3; Gaps 2;  
QY 4 FIDQRAALIAIVTN--VEVLLDALYKG-VLTDEQYQAVRAEPTNPQKRL 52  
DB 438 WIQSKREALVSQMTACLNQSLDALLSRDLINKEDYELISKPTRTSKVRL 489  
RESULT 10  
BIR CHICK  
ID BIR CHICK STANDARD; PRT; 611 AA.  
AC Q90560; O57319;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-NOV-2004 (Rel. 43, Last annotation update)  
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis  
DE protein).  
GN ITA OR IAP1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Splicein;  
EX MEDLINE=97101112; PubMed=8945639;  
RA Digby M.R., Kimpton W.G., York J.J., Connick T.E., Lowenthal J.W.;  
RT "ITA, a vertebrate homologue of IAP that is expressed in T  
RL lymphocytes.";  
RL DNA Cell Biol. 15:981-988(1996).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=White Leghorn; TISSUE=Embryonic fibroblast;  
RA MEDLINE=98038801; PubMed=9372964;  
RX You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;  
RT "ch-IAP1, a member of the inhibitor-of-apoptosis protein family, is a  
RT mediator of the antiapoptotic activity of the v-Rel oncoprotein.";  
RL Mol. Cell. Biol. 17:7328-7341(1997).  
CC -!- FUNCTION: Apoptotic suppressor.  
CC -!- SUBCELLULAR LOCATION: Predominantly nuclear. Cytoplasmic  
CC according to Ref.2.  
CC -!- TISSUE SPECIFICITY: Cells of the T lymphocyte lineage. Found in  
CC both cortical and medullary cells of the thymus. Expressed at  
CC relatively high levels also in spleen, bursa, intestine and lung  
CC and at very low levels in testis, brain and skeletal muscle.  
CC -!- INDUCTION: High levels are induced within 4-8 hours of T-cell  
CC activation in spleen and thymus.  
CC -!- DOMAIN: The ring finger is important for its antiapoptotic effect.  
CC -!- SIMILARITY: Belongs to the IAP family.  
CC -!- SIMILARITY: Contains 3 BIR repeats.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC  
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CC  
CC EMBL; U27466; AAB48118.1; -.  
CC HSSP; Q13490; IQH.  
CC InterPro; IPR001370; BIR.  
CC InterPro; IPR001315; CARD.  
CC InterPro; IPR001841; Znf\_ring.  
CC Pfam; PF00653; BIR; 3.  
CC Pfam; PF00619; CARD; 1.  
CC Pfam; PF00097; zf-C3HC4; 1.  
CC SMART; SM00238; BIR; 3.  
CC SMART; SM00114; CARD; 1.  
CC SMART; SM00184; RING; 1.  
CC PROSITE; PS01282; BIR\_REPEAT\_1; 3.  
CC PROSITE; PS0143; BIR\_REPEAT\_2; 3.  
CC PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
CC PROSITE; PS00089; ZF\_RING\_2; 1.  
CC Apoptosis; Zinc-finger; Repeat; Nuclear protein.  
KW REPEAT 30 97  
FT REPEAT 176 242 BIR 1.  
FT REPEAT 262 329 BIR 2.  
FT REPEAT 446 536 BIR 3.  
FT DOMAIN 564 599 RING-TYPE.  
FT ZN\_FING 27 27 F -> L (IN REF. 2).  
FT CONFLICT 150 150 R -> Q (IN REF. 2).  
FT CONFLICT 169 189 Q -> H (IN REF. 2).  
FT CONFLICT 183 183 S -> F (IN REF. 2).  
FT CONFLICT 190 192 CLW -> FLS (IN REF. 2).  
FT CONFLICT 196 196 V -> L (IN REF. 2).  
FT CONFLICT 202 203 DD -> YY (IN REF. 2).  
FT CONFLICT 213 214 VN -> FT (IN REF. 2).  
FT CONFLICT 217 218 VK -> GO (IN REF. 2).  
FT CONFLICT 350 355 WNSCT -> EQLS (IN REF. 2).  
FT CONFLICT 359 359 K -> T (IN REF. 2).  
FT CONFLICT 426 426 E -> D (IN REF. 2).  
FT CONFLICT 492 492 T -> K (IN REF. 2).  
FT CONFLICT 497 497 S -> L (IN REF. 2).  
FT CONFLICT 524 524 F -> C (IN REF. 2).  
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;  
Query Match 17.6%; Score 66.5; DB 1; Length 611;  
Best Local Similarity 32.7%; Pred. No. 4.4;  
Matches 17; Conservative 14; Mismatches 20; Indels 1; Gaps 1;



QY 2 LHFIQDHRALRIARTVNVENWLLDALY-GKVLTDEQYQAVRAEPTNPSSKRXL 52  
 Db 451 LSLRKNWALPQRLTSVLPILGSLLSAKVTELEHVDHKTOTPPSQAREL 502

RESULT 11

ID	DX52 MOUSE	STANDARD;	PRT;	598 AA.
AC	Q8K3C1; Q8BV29;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	DEAD-box protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase ROK1-like).			
GN	DDX52 OR ROK1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Breast tumor;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Schetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.:			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).			
RL	[2]			
RP	SEQUENCE OF 1-579 FROM N.A.			
RP	STRAIN=C57BL/6J; TISSUE=Retina;			
RC	STRAIN=22354683; PubMed=12466851;			
RC	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustinctich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kawaji H., Kawasaki Y., Lee Y., Lenhard B., Lyons P.A.,			
RA	Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,			
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,			
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,			
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,			
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,			
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,			
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,			
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,			
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,			
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,			

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RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RC Nature 420:563-573 (2002).
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -|- SIMILARITY: Belongs to the DEAD box helicase family.
CC -----
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CC -----
DR EMBL; BC029094; AA29094.1; -.
DR EMBL; AK080767; BAC38014.1; -.
DR MGD; MGI:1925644; Ddx52.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase C; 1.
DR SMART; SMO0487; DEXDC; 1.
DR SMART; SMO0490; HELICC; 1.
DR PROSITE; PS00039; DEAD ATP HELICASE; FALSE NEG.
KW Hydrolyase; Helicase; Nuclear protein; RNA-binding; ATP-binding.
FT NP BIND 210 217
FT SITE 319 322 DEAD BOX.
FT DOMAIN 86 92 POLY-LYS.
FT CONFLICT 75 75 E -> Q (IN REF. 2).
FT CONFLICT 81 81 R -> K (IN REF. 2).
FT CONFLICT 103 103 L -> F (IN REF. 2).
FT CONFLICT 119 119 E -> D (IN REF. 2).
FT CONFLICT 312 312 S -> N (IN REF. 2).
FT CONFLICT 373 373 I -> V (IN REF. 2).
SQ SEQUENCE 598 AA; 67442 MW; 07D825A9F1CFB8DB CRC64;

Query Match 17.2%; Score 65; DB 1; Length 598;
Best Local Similarity 26.0%; Pred.No. 6.4;
Matches 27; Conservative 14; Mismatches 19; Indels 44; Gaps 6;

Qy 2 LHEDIQHRAALIR-----VTNVEWLL----DA 25
Db 266 IHMI-HKAIAAKKFGKSKKFDELVTPNLRIYLKKDDPGCIDITSVEVLVDSDK 323
      :|::||::|:
Qy 26 LY-GKVLTDQOQVAARESTNFSSMKRKLFSFTPAMN---WTCK 64
      :|::|::|:
Db 324 LFEDGKTGFREQLASITFLACTSPKVRAMFSATFYDVDEQW-CK 366
      :|::|::|:

RESULT 12
CAR4 HUMAN
ID _CAR4 HUMAN STANDARD; PRT; 953 AA.
AC Q9Y239; O8IWF5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase recruitment domain protein 4 (Nod1 protein).
GN CARD4 OR NOD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=99240667; PubMed=10224040;
RA Bertin J., Nir W.-J., Fischer C.M., Tayber O.V., Errada P.R.,
RA Grant J.R., Keilty J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,
RA Glucksmann M.A., DiStefano P.S.;
RT "Human CARD4 protein is a novel CED-4/Apaaf-1 cell death family member.
RL That activates NF-kappaB."
RJ J. Biol. Chem. 274:12955-12958(1999).
```

[2] SEQUENCE FROM N.A., AND MUTAGENESIS OF VAL-41 AND LYS-208.  
RP TISSUE=Breast;  
RC MEDLINE=99262599; PubMed=10329646;  
RA Inohara N., Koseki T., del Peso L., Hu Y., Yee C., Chen S., Carrio R.,  
RA Merino J., Liu D., Ni J., Nunez G.;  
RT "Nodal, an Apaf-1-like activator of caspase-9 and nuclear factor-  
kappaB";  
RL J. Biol. Chem. 274:14560-14567(1999).  
[3] SEQUENCE FROM N.A.  
RN TISSUE=Lymph;  
RC MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[4] FUNCTION.  
RP MEDLINE=21264704; PubMed=11058605;  
RA Inohara N., Ogura Y., Chen F.F., Muto A., Nunez G.;  
RT "Human Nod1 confers responsiveness to bacterial lipopolysaccharides";  
RL J. Biol. Chem. 276:2551-2554(2001).  
CC -!- FUNCTION: Enhances caspase-9 mediated apoptosis. Induces NF-kappa-  
B activity via RICK (CARDIAC, RIP2) and IKK-gamma. Confers  
responsiveness to intracellular bacterial lipopolysaccharides  
(LPS).  
CC -!- SUBUNIT: Self-associates. Binds to caspase-9 and RICK by CARD-CARD  
interaction.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: Highly expressed in adult heart, skeletal  
muscle, pancreas, spleen and ovary. Also detected in placenta,  
lung, liver, kidney, thymus, testis, small intestine and colon.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC -!- SIMILARITY: Contains 1 NACHT domain.  
CC -!- SIMILARITY: Contains 9 leucine-rich (LRR) repeats.  
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CC -----  
CC EMBL; AF126484; AAD29125.1; -;  
CC EMBL; AF149774; AAD43922.1; -;  
CC EMBL; AF113925; AAD28350.1; -;  
CC EMBL; BC040339; AAH40339.1; -;  
CC Genbank; HGNC:16390; CARD4.  
CC MIM; 605980; -;  
CC GO; GO:0008656; P:caspase activator activity; TAS.  
CC GO; GO:0006915; P:apoptosis; TAS.  
CC GO; GO:0007165; P:signal transduction; TAS.  
CC InterPro; IPR001315; CARD.  
CC InterPro; IPR007091; LRR\_RNinh.  
CC InterPro; IPR007111; NACHT\_NTPase.

DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF05729; NACHT; 1.  
DR PROSITE; PS0209; CARD; 1.  
DR PROSITE; PS0837; NACHT; 1.  
KW Apoptosis; ATP-binding; Repeat; Leucine-rich repeat.  
FT DOMAIN 15 105  
FT DOMAIN 196 531  
FT NP BIND 202 209  
FT REPEAT 632 656  
FT REPEAT 702 725  
FT REPEAT 727 750  
FT REPEAT 755 778  
FT REPEAT 783 806  
FT REPEAT 839 862  
FT REPEAT 867 891  
FT REPEAT 895 918  
FT REPEAT 923 946  
FT MUTAGEN 41 41  
FT MUTAGEN 208 208  
FT CONFLICT 447 447  
FT SEQUENCE 953 AA; 17690 MW; 0A9DF5FC6487E21A CRC64;  
SQ  
Query Match 17.1%; Score 64.5; DB 1; Length 953;  
Best Local Similarity 28.6%; Pred. No. 12;  
Matches 16; Conservative 12; Mismatches 19; Indels 9; Gaps 2;  
QY 2 LHFIDHRAALIAITVNTVNEVLDAALYGVLTDEQYQAVRAE-----PTNPSQKRL 52  
DB 20 IQLKSNRELLVTHNTQCLVDNL-----LKNDFSAEDAEIVCACPQPKVKRI 71  
RESULT 13  
YCGA\_AERHY STANDARD; PRT; 225 AA.  
ID YCGA\_AERHY  
AC P52047;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 24.5 kDa protein in ahyr-cdpd intergenic region.  
OS Aeromonas hydrophila.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
OC Aeromonadaceae; Aeromonas.  
OX NCBI\_TaxID=644;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A1;  
RX MEDLINE=97431471; PubMed=9286976;  
RA Swift S., Karlyshev A.V., Fish L., Durant E.L., Winson M.K.,  
RA Chhabra S.R., Williams P., Macintyre S., Stewart G.S.A.B.;  
RT Quorum sensing in Aeromonas hydrophila and Aeromonas salmonicida:  
RT Identification of the LuxRI homologs AnyRI and AsaRI and their  
RT cognate N-acylhomoserine lactone signal molecules";  
RL J. Bacteriol. 179:5271-5281(1997).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
CC -!- SIMILARITY: BELONGS TO THE LYSE/YCGA FAMILY.  
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CC -----  
CC EMBL; X89469; CAA61655.1; ALT\_INIT.  
CC InterPro; IPR004777; Lys\_exporter.  
CC InterPro; IPR001123; LYSE.  
CC Pfam; PF01810; LYSE; 1.  
CC TIGRFAMs; TIGR00948; 2a75; 1.  
CC Hypothetical protein; Transmembrane.  
FT TRANSMEM 1 21  
FT TRANSWEM 37 57  
POTENTIAL.

FT TRANSMEM 65 85 POTENTIAL.  
FT TRANSMEM 116 136 POTENTIAL.  
FT TRANSMEM 150 170 POTENTIAL.  
SQ SEQUENCE 225 AA; 24482 MW; 172DB104473B0B09 CRC64;  
  
Query Match 16.5%; Score 62.5; DB 1; Length 225;  
Best Local Similarity 24.6%; Pred. No. 4.3;  
Matches 16; Conservative 11; Mismatches 33; Indels 5; Gaps 2;  
  
QY 1 GLHFIDQHRAL--IARVTNVEMLLDALYGVLTDEQYQAVRAEPNPSKVKLFSFTPA 58  
Db 137 GSQFAEELRSFAFAMVAMSLWFWYSLAFGAVLSPWLARSR---QGYSKLLILLVSPC 193  
  
QY 59 WNWTC 63  
Db 194 WGNRC 198  
  
RESULT 14  
RIK2 HUMAN  
ID -RIK2 HUMAN STANDARD; PRT; 540 AA.  
AC O43353;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.37)  
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme  
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase).  
GN RIPK2 OR RICK OR RIP2 OR CARDIAK.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RX MEDLINE=98241596; Pubmed=9575181;  
RI Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;  
RT "RICK, a novel protein kinase containing a caspase recruitment domain,  
RT interacts with CARD and regulates CD95-mediated apoptosis.";  
RL J. Biol. Chem. 273:122296-12300(1998).  
[2]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.  
RC TISSUE=Endothelial cells;  
RX MEDLINE=98307936; Pubmed=9642260;  
RA McCarthy J.V., Ni J., Dixit V.M.;  
RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing  
RT kinase.";  
RL J. Biol. Chem. 273:16968-16975(1998).  
[3]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-145.  
RX MEDLINE=98381580; Pubmed=3703936;  
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,  
RA Mattmann C., Tschopp J.;  
RT "Identification of CARDIAK, a RIP-like kinase that associates with  
RT caspase-1.";  
RL Curr. Biol. 8:885-888(1998).  
[4]  
RP SEQUENCE FROM N.A.  
RA Ozersky P., Holmes A., Brody M.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE FROM N.A.  
RA Platzner M., Varon R.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
[6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=23388257; Pubmed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates  
CC CASP-8-mediated apoptosis. Activates NF-kappaB.  
CC -!- SUBUNIT: Binds to CFLAR/CARP and CASP1 via their CARD domains.  
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF3 and  
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40  
CC receptor complex.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
CC -!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,  
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,  
CC pancreas and lymph node.  
CC -!- PTM: Autophosphorylated.  
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.  
CC -!- SIMILARITY: Contains 1 CARD domain.  
CC -----  
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CC -----  
DR EMBL; AF027706; AAC34970.1; -;  
DR EMBL; AF078530; AAC27722.1; -;  
DR EMBL; AF064824; AAC25668.1; -;  
DR EMBL; AC004003; AAC24561.1; -;  
DR EMBL; AF117829; RAD04634.1; -;  
DR EMBL; BC004553; AAH04553.1; -;  
DR Genew; HGNC:10020; RIPK2.  
DR MIM; 603455; -;  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.  
DR GO; GO:0004871; F:signal transducer activity; TAS.  
DR GO; GO:0006915; P:apoptosis; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR001315; CARD.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_Thr\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00619; CARD; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00114; CARD; 1.  
DR PROSITE; PS00209; CARD; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation; Apoptosis.  
FT DOMAIN 18 294 PROTEIN KINASE.  
FT DOMAIN 432 524 CARD.  
FT NP\_BIND 24 32 ATP (BY SIMILARITY).  
FT BINDING 47 47 ATP.  
FT ACT\_SITE 146 146  
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.

Job time : 7.84337 secs

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FT MUTAGEN 47 47 K->M: REDUCES FAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA: 61194 MW; 575A692239505792 CRC64;

Query Match 16.5%; Score 62.5; DB 1; Length 540;
Best Local Similarity 30.4%; Pred. No. 11;
Matches 17; Conservative 13; Mismatches 23; Indels 3; Gaps 2;

QY 4 FIDQHRALIAIARVTN--VEWLLDALYK-VLTDEQYQAVRAEPTNPCKMLFSFT 56
Db 439 WIQSKREDIVNQMTBACLNSLDLSSRLDKEDYELVSTKPTKTKVQLDDTT 494

RESULT 15
DX52_RAT
ID DX52 RAT STANDARD; PRT; 598 AA.
AC Q99PT0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DEAD-box protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase
DE ROKI-like) (PROKIL).
GN DX52 OR ROK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Li W., Suzuki T.;
RT "Identification of a novel ROKI-like protein in rat brain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -!- SIMILARITY: Belongs to the DEAD box helicase family.
CC -----
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CC -----
CC EMBL; AB055628; BAB32441.1; -.
CC HSP; Q58083; 1HV8.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR001850; Helicase_C.
CC Pfam; PF00270; DEAD; 1.
CC Pfam; PF00271; Helicase_C; 1.
CC SMART; SM00487; DEXDC; 1.
CC SMART; SM00490; HELICC; 1.
CC PROSITE; PS00039; DEAD_ATP_HELICASE; FALSE NEG.
KW Hydrolase; Helicase; Nuclear protein; RNA-binding; ATP-binding.
FT NP_BIND 210 217 ATP (BY SIMILARITY).
FT SITE 319 322 DEAD BOX.
FT DOMAIN 86 92 POLY-LYS.
SQ SEQUENCE 598 AA: 67239 MW; B9E818EA6B14425 CRC64;

Query Match 16.4%; Score 62; DB 1; Length 598;
Best Local Similarity 25.0%; Pred. No. 14;
Matches 26; Conservative 15; Mismatches 19; Indels 44; Gaps 6;

QY 2 LHFIDQHRALIAIAR-----VTNVEWLL----DA 25
Db 266 IHMI--HKAIAAKKFGPKSKKFDILVTTPNRLIYLKQPPGIDLTSEVLVVDSDK 323

QY 26 LY--CKVLTDEQYQAVRAEPTNPCKMLFSFTPAWN---WTCK 64
Db 324 LFEDGKTGFRDQLASIFLACTSPKVRRAWFATFAYDVEQW-CK 366
```

Search completed: July 28, 2004, 08:53:28

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 08:49:47 ; Search time 28.2289 Seconds  
(without alignments)  
793.576 Million cell updates/sec

Title: US-09-996-617-8\_COPY\_111\_181

Perfect score: 378

Sequence: 1 GLHFIDQRAALIARTVNE.....LRSFPAWNWTKDLLLQAL 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	80.2	195	6 Q8HKK9	Q8HKK9 bos taurus
2	269	71.2	193	11 Q8CHK8	Q8CHK8 rattus norv
3	73.5	19.4	220	11 Q8C550	Q8C550 mus musculus
4	69.5	18.4	220	11 Q8R283	Q8R283 mus musculus
5	68	18.0	449	16 Q88WC4	Q88WC4 lactobacill
6	68	18.0	545	16 Q9CBL2	Q9CBL2 mycobacteri
7	67	17.7	257	4 Q9H695	Q9H695 homo sapien
8	67	17.7	912	15 Q90278	Q90278 chimpanzee
9	67	17.7	1175	16 Q8XNW6	Q8XNW6 cleistridium
10	66.5	17.6	1170	16 Q882B7	Q882B7 pseudomonas
11	66	17.5	249	4 Q8N528	Q8N528 homo sapien
12	65.5	17.3	149	16 Q8FTY0	Q8FTY0 corynebacte
13	65.5	17.3	616	13 Q804E2	Q804E2 ictalurus p
14	65.5	17.3	628	13 Q8UWD2	Q8UWD2 brachydanio
15	65.5	17.3	647	13 Q7TOK2	Q7TOK2 brachydanio
16	65	17.2	1134	16 Q8PEL2	Q8PEL2 xanthomonas

17	64.5	17.1	597	10 Q9ZSB8	Q9ZSB8 arabidopsis
18	64.5	17.1	605	10 Q9T0C0	Q9T0C0 arabidopsis
19	64	16.9	304	16 Q9PU91	Q9PU91 campylobact
20	63.5	16.8	285	16 Q8PEI0	Q8PEI0 xanthomonas
21	63.5	16.8	456	13 Q9W7D6	Q9W7D6 oryzias lat
22	63	16.7	565	2 Q9KJ20	Q9KJ20 actinopolys
23	63	16.7	955	16 Q8A654	Q8A654 bacteroides
24	63	16.7	1134	16 Q8P378	Q8P378 xanthomonas
25	62.5	16.5	602	11 Q9SEB9	Q9SEB9 rattus norv
26	62.5	16.5	610	13 Q57319	Q57319 gallus gall
27	62	16.4	779	16 Q8YN00	Q8YN00 anabaena sp
28	61.5	16.3	128	2 Q8GHU3	Q8GHU3 pseudomonas
29	61.5	16.3	280	16 Q8P342	Q8P342 xanthomonas
30	61.5	16.3	306	5 Q19619	Q19619 caenorhabdi
31	61.5	16.3	650	2 Q52870	Q52870 rhizobium 1
32	61.5	16.3	1193	5 Q19617	Q19617 caenorhabdi
33	61.5	16.3	3729	2 Q33956	Q33956 streptomyce
34	61	16.1	277	16 Q916Q4	Q916Q4 pseudomonas
35	61	16.1	321	11 Q8BUR0	Q8BUR0 mus musculu
36	61	16.1	326	16 Q9KZK7	Q9KZK7 streptomyce
37	61	16.1	338	16 Q8ZDY2	Q8ZDY2 yersinia pe
38	61	16.1	342	11 Q8D818	Q8D818 mus musculu
39	61	16.1	345	12 Q84439	Q84439 parametium
40	61	16.1	353	16 Q82NU4	Q82NU4 streptomyce
41	61	16.1	359	11 Q9DJN8	Q9DJN8 mus musculu
42	61	16.1	666	2 Q9RHG7	Q9RHG7 bacillus ce
43	61	16.1	983	2 Q9KDX6	Q9KDX6 bacillus me
44	61	16.1	983	2 Q93R39	Q93R39 bacillus ce
45	60.5	16.0	290	11 Q921C9	Q921C9 cricetulus

#### ALIGNMENTS

#### RESULT 1

ID Q8HKK9 PRELIMINARY; PRT; 195 AA.

AC Q8HKK9;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Apoptosis-associated speck-like protein containing a CARD.

GN BASC.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

OX [1]

RN SEQUENCE FROM N.A.

RA Masumoto J., Zhou W., Chen F.F., Su F., Kuwada J.Y., Hidaka E.,

RA Katsuyama T., Sagara J., Taniguchi S., Nigo-Hazelett P.,

RA Postlethwait J.H., Nunez G., Inohara N.,

RT "Casp-1: A Zebrafish caspase activated by ASC oligomerization required

RT for pharyngeal Arch development.";

RL J. Biol. Chem. 0:0-0(2002).

RN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=20036508; PubMed=10567338;

RA Masumoto J., Taniguchi S., Ayukawa K., Sarvotham H., Kishino T.,

RA Niiikawa N., Hidaka E., Katsuyama T., Higuchi T., Sagara J.,

RT "ASC, a novel 22-kDa protein, aggregates during apoptosis of human

RT promyelocytic leukemia HL-60 cells.";

RL J. Biol. Chem. 274:33835-33838(1999).

RN [3]

RN SEQUENCE FROM N.A.

RP MEDLINE=20580347; PubMed=11139337;

RA Masumoto J., Taniguchi S., Nakayama K., Ayukawa K., Sagara J.,

RT "Murine ortholog of ASC, a CARD-containing protein, self-associates,

RT and exhibits restricted distribution in developing mouse embryos.";

RL Exp. Cell Res. 262:128-133(2001).

DR EMBL; AB050006; BAC43753.1; -.

DR GO; GO:0005622; C:intracellular; IEA.



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OY 57 -----PANW 61
DB 72 ACQELLRCQQTVMPPDPAWD 93

RESULT 5
Q88WC4 PRELIMINARY; PRT; 449 AA.
AC Q88WC4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Amino transferase (EC 2.6.1.-).
GN Lp1721.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Stenzen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBL; AL932527; CAD64145.1; -.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; aminotran_3; 1.
DR Amino transferase; Transferase; Complete proteome.
KW Amino transferase; Transferase; Complete proteome.
SQ SEQUENCE 449 AA; 49491 MW; E2CD4FE25F69E0C CRC64;

Query Match 18.0%; Score 68; DB 16; Length 449;
Best Local Similarity 27.2%; Pred. No. 7.7;
Matches 22; Conservative 13; Mismatches 22; Indels 24; Gaps 4;

OY 3 HFIDQ-----HRAALIARTVNVWMLDALYGVLT-----EQY-----QAVRAEPTN 45
DB 6 HRLDQQLIEREDHYMATAIRYNYDLVIDHAGALLTVDGNGQYIDLLASASAINVGHTH 65

OY 46 PSKMR-----KLFSFTPAW 59
DB 66 PRVVAIQEQAKLIHTIPAY 86

RESULT 6
Q9CBL2 PRELIMINARY; PRT; 545 AA.
AC Q9CBL2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ABC transporter ATP-binding protein, possibly in EF-3 subfamily.
GN Ml1816.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
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RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
EMBL; AL583923; CAC30769.1; -.
DR PIR; A87136; A87136.
DR Leproma; MLI816; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 545 AA; 58986 MW; 75AAA463EB91FBCD CRC64;

Query Match 18.0%; Score 68; DB 16; Length 545;
Best Local Similarity 36.4%; Pred. No. 9.7;
Matches 20; Conservative 3; Mismatches 16; Indels 16; Gaps 2;

OY 8 HRAALIARTVNVWMLDALYGV-----LTDEYQAVRAEPTNPSK 48
DB 226 HNVELIAAVNRVWFLDAVLGKVDYVNGWYKYLDSRATDQRR--RRERVNAER 278

RESULT 7
Q9H695 PRELIMINARY; PRT; 257 AA.
AC Q9H695;
DT 01-VAR-2001 (TREMBlrel. 16, Created)
DT 01-VAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein FLJ22474.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Oabayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.
EMBL; AK026127; BAB15368.1; -.
DR Genew; HGNC:20310; GRTPI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000195; RabGAP_TBC.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR PROSITE; PS00866; TBC_RABGAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 257 AA; 28960 MW; 5B0A7B5779DF2B94 CRC64;

Query Match 17.7%; Score 67; DB 4; Length 257;
Best Local Similarity 33.9%; Pred. No. 5.2;
Matches 19; Conservative 10; Mismatches 19; Indels 8; Gaps 2;

OY 1 GLHFIDQHRAALIARTVNV-----WLDALYGVLTDEYQAVRAEPTNPSKVKL 52
DB 69 GNMFT----AGYLVLTITNNEESFWLLDALVGRILPDYSPAMGLKTDQEVIGEL 120
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RESULT 8
OS0278 PRELIMINARY; PRT; 912 AA.
ID O90278
AC O90278;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope protein.
GN ENV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SV11hoest;
RX MEDLINE=99098990; PubMed=9882304;
RA Hirsch V.M., Campbell B.J., Bailes E., Goeken R., Brown C.,
RA Elkins W.R., Athelm M., Murphey-Corb M., Sharp P.M.;
RT "Characterization of a novel simian immunodeficiency virus (SIV) from
RT L'Hoest monkeys (Cercopithecus l'hoesti): implications for the origins
RT of SIVmd and other primate lentiviruses.";
RL J. Virol. 73:1036-1045(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SV11hoest;
RA Hirsch V.M.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075269; RAD12149.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 912 AA; 104904 MW; 70FBE016922DAAC CRC64;

Query Match 17.7%; Score 67; DB 15; Length 912;
Best Local Similarity 29.0%; Pred. No. 24;
Matches 18; Conservative 7; Mismatches 19; Indels 18; Gaps 2;

QY 17 TNVEWLD-----ALYKVLTEQYQAVRAEPTNSKMRKLPSPFPAP 59
D5 642 TNVEYTNITPNTWTDWREWSKVAIYDKNITSLLQEAYTTELENGKFKLQEFN-FW 700
QY 60 NW 61
D5 701 SW 702

RESULT 9
OSXNW6 PRELIMINARY; PRT; 1175 AA.
ID OSXNW6
AC OSXNW6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Probable exonuclease.
GN SBCC OR CPE0216.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A; PubMed=11792842;
RX MEDLINE=21664373; PubMed=21664373;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic

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RT flesh-eater.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003185; BAB7922.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
DR GO; GO:0004527; F:exonuclease activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
KW Exonuclease; Complete proteome.
SQ SEQUENCE 1175 AA; 138878 MW; 7C6D2366525019C1 CRC64;

Query Match 17.7%; Score 67; DB 16; Length 1175;
Best Local Similarity 36.2%; Pred. No. 33;
Matches 17; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 5 IQCHRAALIAITVNVWLLDALYKVLTEQYQAVRAEPTNSKMRK 51
D5 924 IBEYNNLIKIKANIELLIKNGKSLTEEWTRVLQKNTERELK 970

RESULT 10
OS82B7 PRELIMINARY; PRT; 1170 AA.
ID Q882B7
AC Q882B7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sensor histidine kinase/response regulator.
DR PSPT02712.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collmer A.;
RT "Complete sequence of Pseudomonas syringae.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS018665; AA056213.1; -.
DR TIGR; PSPT02712; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact sens_pr_C.
DR InterPro; IPR007891; CHASE3.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF05227; CHASE3; 1.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF00072; response reg; 3.
DR PRINTS; PR00344; BCTLSNSOR.
DR PROSITE; PS00214; FAMP; 1.

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RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RW ENBL: AP005214; BAC17053.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 149 AA; 16334 MW; D11861ADB491A4F5 CRC64;

Query Match 17.3%; Score 65.5; DB 16; Length 149;
Best Local Similarity 32.7%; Pred. No. 4.1;
Matches 17; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QHRAALIAITVNV -WLIDALYKGLTDEQYCAVRAEPTNPCKMRKLPST 56
Db 99 QHKSASIASTELSHLWISASTQILAD-TYSVIFADDSVENIMRRTFGWT 149

RESULT 13
Q804E2 PRELIMINARY; PRT; 616 AA.
ID Q804E2
AC Q804E2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein-1.
GN CIAP-1.
GS Itcalurus punctatus (Channel catfish).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Itcaluridae; Itcalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Praveen K., Leary J.H. III, Evans D.L., Jaso-Friedmann L.;
RL "Cloning of anti-apoptotic genes in non-specific cytotoxic cells.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY184377; AAC24632.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008189; F:apoptosis inhibitor activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00114; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PSS0209; CARD; 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
SQ SEQUENCE 616 AA; 69546 MW; D1389D915C6BB256 CRC64;

Query Match 17.3%; Score 65.5; DB 13; Length 616;
Best Local Similarity 34.1%; Pred. No. 23;
Matches 14; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Qy 1 GLHFIDQHRALIAITVNVWLLDALYK-VLTDEQYQAVR 40
Db 455 GFTFLKHHALTORLSKVSQSLMDHLEENVISQKEDTIR 495

RESULT 14
Q8UWD2 PRELIMINARY; PRT; 628 AA.
ID Q8UWD2
AC Q8UWD2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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